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OM protein - protein search, using sw model

Run on: January 30, 2003, 13:31:57 ; Search time 35 Seconds
(without alignments)
38.072 Million cell updates/sec

Title: US-09-615-624A-1

Perfect score: 59

Sequence: 1 CRLSGEPQC 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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12: /SID22/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:*
13: /SID22/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:*
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21: /SID22/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
22: /SID22/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
23: /SID22/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|-------------|--------------------|
| 1 | 59 | 100.0 | 10 | 22 AAB46753 | MMP-9 antagonist p |
| 2 | 45 | 76.3 | 10 | 22 AAB46754 | MMP-9 antagonist p |
| 3 | 42 | 71.2 | 2091 | 22 ABB70224 | Drosophila melanog |
| 4 | 41 | 69.5 | 798 | 22 AAB39360 | Human polypeptide |
| 5 | 41 | 69.5 | 798 | 22 AAB36937 | Human integrin bet |
| 6 | 41 | 69.5 | 805 | 22 AAM41146 | Human polypeptide |
| 7 | 41 | 69.5 | 963 | 19 AA470540 | Integrin beta-1 ch |
| 8 | 40 | 67.8 | 62 | 22 ABG29623 | Novel human diagno |
| 9 | 40 | 67.8 | 145 | 22 ABG21707 | Novel human diagno |
| 10 | 40 | 67.8 | 191 | 22 ABG21688 | Novel human diagno |

| | | | | | | |
|----|------|------|------|----|-----------|---------------------|
| 11 | 40 | 67.8 | 205 | 22 | ABG21679 | Novel human diagno |
| 12 | 40 | 67.8 | 207 | 22 | ABG21676 | Novel human diagno |
| 13 | 40 | 67.8 | 247 | 22 | ABG21675 | Novel human diagno |
| 14 | 40 | 67.8 | 257 | 22 | ABG21680 | Novel human diagno |
| 15 | 40 | 67.8 | 1043 | 22 | ABG06467 | Novel human diagno |
| 16 | 39 | 66.1 | 10 | 22 | ABG46755 | MMP-9 antagonist p |
| 17 | 39 | 66.1 | 110 | 22 | AAAM38902 | Human polypeptide |
| 18 | 39 | 66.1 | 179 | 12 | AAAL15426 | Bovine epithelin p |
| 19 | 39 | 66.1 | 228 | 22 | AAAM40688 | Human polypeptide |
| 20 | 38.5 | 65.3 | 163 | 22 | AAAM88487 | Human ribonuclease |
| 21 | 38 | 64.4 | 17 | 21 | AAAB52042 | Human secreted pro |
| 22 | 38 | 64.4 | 157 | 22 | AAAB70321 | Drosophila melanog |
| 23 | 38 | 64.4 | 230 | 22 | ABG25277 | Novel human diagno |
| 24 | 38 | 64.4 | 345 | 21 | AAAB01456 | PML mutant polypep |
| 25 | 38 | 64.4 | 358 | 11 | AAAR05123 | Bat-PA(L). Desmod |
| 26 | 38 | 64.4 | 367 | 21 | AAAB01455 | PML mutant polypep |
| 27 | 38 | 64.4 | 394 | 11 | AAAR06486 | v-PA-gamma. Desmo |
| 28 | 38 | 64.4 | 395 | 11 | AAAR05125 | Modified Bat-PA(H) |
| 29 | 38 | 64.4 | 431 | 11 | AAAR06459 | v-PA_beta. Desmod |
| 30 | 38 | 64.4 | 477 | 11 | AAAR05122 | Bat-PA(H). Desmod |
| 31 | 38 | 64.4 | 477 | 11 | AAAR05122 | Bat-PA(H). Desmod |
| 32 | 38 | 64.4 | 560 | 13 | AAAR27535 | myl protein. Synt |
| 33 | 38 | 64.4 | 560 | 20 | AAW81965 | Human myl-1 protel |
| 34 | 38 | 64.4 | 797 | 13 | AAAR27533 | myl/RAR-alpha fusi |
| 35 | 38 | 64.4 | 797 | 20 | AAW81963 | Human myl/RAR-alpha |
| 36 | 38 | 64.4 | 798 | 23 | ABBS7079 | Mouse ischaemic co |
| 37 | 38 | 64.4 | 819 | 22 | ABG18860 | Novel human diagno |
| 38 | 37 | 62.7 | 71 | 20 | AAAY05202 | Human FCMF follist |
| 39 | 37 | 62.7 | 159 | 22 | AAAM87880 | Human immune/haema |
| 40 | 37 | 62.7 | 206 | 21 | AAAB32113 | Human secreted pro |
| 41 | 37 | 62.7 | 263 | 20 | AAAY14571 | Human apoptosis in |
| 42 | 37 | 62.7 | 263 | 20 | AAAY06201 | Follistatin module |
| 43 | 37 | 62.7 | 263 | 20 | AAAY01098 | Human follistatin- |
| 44 | 37 | 62.7 | 263 | 22 | AAAU12413 | Human PRO1308 poly |
| 45 | 37 | 62.7 | 263 | 22 | AAAY72875 | Human PRO1308 prot |

ALIGNMENTS

RESULT 1
AAB46753
ID AAB46753 standard; peptide; 10 AA.
XX
AC AAB46753;
XX
DT 12-APR-2001 (first entry)
XX
DE MMP-9 antagonist peptide FRIP-1.
XX
KW Antagonist; MMP-9; inhibition; angiogenesis; tumor growth; beta-integrin;
KW protein-protein interaction; matrix metalloproteinase; cytosolic; sarcoma;
KW antitumor; antiproliferative; vasotropic; antidiabetic; osteopathic; glioma;
KW anti-rheumatoid; antiarthritic; antithrombotic; antithrombotic; ophthalmological;
KW antiinflammatory; metastasis; psoriasis; macular degeneration;
KW neurological disease; testis; melanoma; carcinoma; fibrosarcoma;
KW astrocytoma; diabetic retinopathy; neovascular glaucoma; osteoporosis;
KW atherosclerotic plaques; rheumatoid arthritis.
OS Synthetic.
XX
XX WO200104157-A2.
XX
PD 18-JAN-2001.
XX
PF 13-JUL-2000; 2000WO-US19095.
XX
PR 13-JUL-1999; 99US-0143581.
XX
PR 02-SEP-1999; 99US-0152495.
XX
PA (UWSC-) UNIV SOUTHERN CALIFORNIA.
XX
PI Brooks PC, Hassanieh L, Rodriguez D;

XX DR WPI; 2001-138319/14.

XX PN Novel antagonist inhibiting angiogenesis by modifying protein-protein

PT interactions, specifically matrix metalloproteinase-9 - beta1 containing

PT integrin interaction, useful to inhibit psoriasis, macular degeneration

PT

XX

XX Claim 27; Page 60; 61pp; English.

XX This invention describes a novel antagonist (I) that inhibits

CC angiogenesis and/or tumor growth by modifying protein-protein

CC interactions which specifically binds to matrix metalloproteinase (MMP)-9

CC or beta-1 integrin. The products of the invention have cytostatic,

CC antitumor, antipsoriatic, vasotropic, antidiabetic, osteopathic,

CC anti-rheumatoid, antiarthritic, antiatherosclerotic, ophthalmological and

CC antiinflammatory activity. (I) inhibits angiogenesis, tumor growth,

CC neurological disease, or restenosis in a tissue. (I) is useful for

CC inhibiting angiogenesis, in a mammalian arthritic, ocular, retinal, or

CC hemangioma tissue which is inflamed and angiogenesis is occurring. (I) is

CC also useful for inhibiting tumor growth or metastasis such as melanoma,

CC carcinoma, sarcoma, fibrosarcoma, glioma, or astrocytoma, in a tissue.

CC (I) is also useful for inhibiting psoriasis, macular degeneration or

CC restenosis in a tissue. In all the above conditions, (I) is administered

CC in conjunction with chemotherapy or radiation. (I) is also useful for

CC detecting angiogenesis and detecting tumors or tumor invasion in a tissue

CC ex vivo. The antagonist in this case is conjugated to fluorochrome,

CC radioactive tag, paramagnetic heavy metal, diagnostic dye or enzyme. (I)

CC is also useful for treating diabetic retinopathy, neovascular glaucoma,

CC atherosclerotic plaques, osteoporosis, rheumatoid arthritis and other

CC inflammatory diseases. The method are effective in part because the

CC therapy is highly selective for angiogenesis and no other biological

CC processes. Only new vessel growth is inhibited by antagonists that

CC disrupt the localization of MMP-9, and therefore the therapeutic methods

CC do not adversely effect mature vessels. Also, because certain of (I)

CC affect only the localization of MMP-9, and do not directly block the

CC proteolytic activity of MMP-9 or the adhesive functions of the beta1

CC integrins, it is likely that these compounds will have fewer side effects

CC because the proteolytic activity of MMP-9 or the adhesive functions of

CC the beta1 integrins may have normal physiological functions. The

CC antagonists are highly potent suggesting that they may have therapeutic

CC benefits at low concentrations.

XX

SQ Sequence 10 AA;

Query Match 100.0%; Score 59; DB 22; Length 10;

Best Local Similarity 100.0%; Pred. No. 0.0028;

Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 CRLRSGEPQC 10

Db 1 CRLRSGEPQC 10

RESULT 2

AAB46754

ID AAB46754 standard; peptide; 10 AA.

XX

AC AAB46754;

XX

DT 12-APR-2001 (first entry)

XX

DE MMP-9 antagonist peptide AAA.

XX

KW Antagonist; MMP-9; inhibition; angiogenesis; tumor growth; beta-integrin;

KW protein-protein interaction; matrix metalloproteinase; cytostatic; sarcoma;

KW antitumor; antipsoriatic; vasotropic; antidiabetic; osteopathic; glioma;

KW anti-rheumatoid; antiarthritic; antiatherosclerotic; ophthalmological;

KW antiinflammatory; metastasis; psoriasis; macular degeneration;

KW neurological disease; restenosis; melanoma; carcinoma; fibrosarcoma;

KW astrocytoma; diabetic retinopathy; neovascular glaucoma; osteoporosis;

KW atherosclerotic plaques; rheumatoid arthritis.

XX OS Synthetic.

XX WO200104157-A2.

XX PN

XX PD 18-JAN-2001.

XX

XX PF 13-JUL-2000; 2000WO-US19095.

XX

XX PR 13-JUL-1999; 99US-0143581.

XX PR 02-SEP-1999; 99US-0152495.

XX

XX (UYSC-) UNIV SOUTHERN CALIFORNIA.

XX

XX Brooks PC, Hassanieh L, Rodriguez D;

XX WPI; 2001-138319/14.

XX

XX Novel antagonist inhibiting angiogenesis by modifying protein-protein

XX interactions, specifically matrix metalloproteinase-9 - beta1 containing

XX integrin interaction, useful to inhibit psoriasis, macular degeneration

XX

XX Example 7; Page 60; 61pp; English.

XX This invention describes a novel antagonist (I) that inhibits

CC angiogenesis and/or tumor growth by modifying protein-protein

CC interactions which specifically binds to matrix metalloproteinase (MMP)-9

CC or beta-1 integrin. The products of the invention have cytostatic,

CC antitumor, antipsoriatic, vasotropic, antidiabetic, osteopathic,

CC anti-rheumatoid, antiarthritic, antiatherosclerotic, ophthalmological and

CC antiinflammatory activity. (I) inhibits angiogenesis, tumor growth,

CC metastasis, or a disease state such as psoriasis, macular degeneration,

CC neurological disease, or restenosis in a tissue. (I) is useful for

CC inhibiting angiogenesis, in a mammalian arthritic, ocular, retinal, or

CC hemangioma tissue which is inflamed and angiogenesis is occurring. (I) is

CC also useful for inhibiting tumor growth or metastasis such as melanoma,

CC carcinoma, sarcoma, fibrosarcoma, glioma, or astrocytoma, in a tissue.

CC (I) is also useful for inhibiting psoriasis, macular degeneration or

CC restenosis in a tissue. In all the above conditions, (I) is administered

CC in conjunction with chemotherapy or radiation. (I) is also useful for

CC detecting angiogenesis and detecting tumors or tumor invasion in a tissue

CC ex vivo. The antagonist in this case is conjugated to fluorochrome,

CC radioactive tag, paramagnetic heavy metal, diagnostic dye or enzyme. (I)

CC is also useful for treating diabetic retinopathy, neovascular glaucoma,

CC atherosclerotic plaques, osteoporosis, rheumatoid arthritis and other

CC inflammatory diseases. The method are effective in part because the

CC therapy is highly selective for angiogenesis and no other biological

CC processes. Only new vessel growth is inhibited by antagonists that

CC disrupt the localization of MMP-9, and therefore the therapeutic methods

CC do not adversely effect mature vessels. Also, because certain of (I)

CC affect only the localization of MMP-9, and do not directly block the

CC proteolytic activity of MMP-9 or the adhesive functions of the beta1

CC integrins, it is likely that these compounds will have fewer side effects

CC because the proteolytic activity of MMP-9 or the adhesive functions of

CC the beta1 integrins may have normal physiological functions. The

CC antagonists are highly potent suggesting that they may have therapeutic

CC benefits at low concentrations.

XX

SQ Sequence 10 AA;

Query Match 76.3%; Score 45; DB 22; Length 10;

Best Local Similarity 70.0%; Pred. No. 0.57;

Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 1 CRLRSGEPQC 10

Db 1 CRAAGEPQC 10

RESULT 3

ABB70224

ID ABB70224 standard; Protein; 2091 AA.

```

XX AC ABB70224;
XX DT 26-MAR-2002 (first entry)
XX DE Drosophila melanogaster polypeptide SEQ ID NO 37464.
XX KW Drosophila; developmental biology; cell signalling; insecticide;
XX KW pharmaceutical.
XX OS Drosophila melanogaster.
XX PN WO200171042-A2.
XX PD 27-SEP-2001.
XX PF 23-MAR-2001; 2001WO-US09231.
XX PR 23-MAR-2000; 2000US-191637P.
XX PR 11-JUL-2000; 2000US-0614150.
XX PA (PEKE ) PE CORP NY.
XX PI Venter JC, Adams M, Li PWD, Myers EW;
XX PI WPI; 2001-656860/75.
XX DR N-PSDB; ABL14327.
XX DR
XX PT New isolated nucleic acid detection reagent for detecting 1000 or more
XX PT genes from Drosophila and for elucidating cell signalling and cell-cell
XX PT interactions.
XX PS Disclosure; SEQ ID NO 37464; 21pp + Sequence Listing; English.
XX CC The invention relates to an isolated nucleic acid detection reagent
XX CC capable of detecting 1000 or more genes from Drosophila. The invention is
XX CC useful in developmental biology and in elucidating cell signalling and
XX CC cell-cell interactions in higher eukaryotes for the development of
XX CC insecticides, therapeutics and pharmaceutical drugs. The invention
XX CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
XX CC sequences (ABL01840-ABL16175) and the encoded proteins
XX CC (ABB57737-ABB72072).
XX CC The sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic format directly from WIPO
XX CC at ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 2091 AA;
Query Match 71.2%; Score 42; DB 22; Length 2091;
Best Local Similarity 88.9%; Pred. No. 2.3e+02;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 CRLRSGEPQ 9
Db 1632 CRLRSGEAQ 1640
|||||||
RESULT 4
AAM39360
ID AAM39360 standard; Protein; 798 AA.
XX AC AAM39360;
XX DT 22-OCT-2001 (first entry)
XX DE Human polypeptide SEQ ID NO 2505.
XX KW Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer;
XX KW peripheral nervous system; neuropathy; central nervous system; CNS;
XX KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
XX KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
XX KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
XX KW leukaemia.
XX OS Homo sapiens.
XX OS
XX PN WO200153312-A1.
XX PD 26-JUL-2001.
XX PF 26-DEC-2000; 2000WO-US34263.
XX PR 21-JAN-2000; 2000US-0488725.
XX PR 25-APR-2000; 2000US-0552317.
XX PR 09-JUL-2000; 2000US-0598042.
XX PR 19-JUL-2000; 2000US-0620312.
XX PR 03-AUG-2000; 2000US-0653450.
XX PR 14-SEP-2000; 2000US-0662191.
XX PR 19-OCT-2000; 2000US-0693036.
XX PR 29-NOV-2000; 2000US-0727344.
XX PA (HYSE-) HYSEQ INC.
XX PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
XX PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
XX PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;
XX DR WPI; 2001-442253/47.
XX DR N-PSDB; AAI58516.
XX PT Novel nucleic acids and polypeptides, useful for treating disorders
XX PT such as central nervous system injuries.
XX PS Example 4; SEQ ID NO 2505; 10078pp; English.
XX CC The invention relates to human nucleic acids (AAI57798-AAI61369) and
XX CC the encoded polypeptides (AAM3642-AAM42213) with nootropic,
XX CC immunosuppressant and cytostatic activity. The polynucleotides are useful
XX CC in gene therapy. A composition containing a polypeptide or polynucleotide
XX CC of the invention may be used to treat diseases of the peripheral nervous
XX CC system, such as peripheral nervous injuries, peripheral neuropathy and
XX CC localised neuropathies and central nervous system diseases, such as
XX CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
XX CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
XX CC utilisation of the activities such as: Immune system suppression,
XX CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
XX CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
XX CC assays for receptor activity, arthritis and inflammation, leukaemias and
XX CC C.N.S disorders.
XX CC Note: the sequence data for this patent did not form part of the printed
XX CC specification.
XX SQ Sequence 798 AA;
Query Match 69.5%; Score 41; DB 22; Length 798;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 RLRSGEQP 9
Db 122 RLRSGEQP 129
|||||||
RESULT 5
AAB36937
ID AAB36937 standard; protein; 798 AA.
XX AC AAB36937;
XX DT 27-FEB-2001 (first entry)
XX DE Human integrin beta 1 subunit.
XX KW Tenascin-C; axon; dendrite; neurite.
XX OS Homo sapiens.

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XX WO2000066628-A1.
XX 09-NOV-2000.
XX 28-APR-2000; 2000WO-US11647.
XX 01-MAY-1999; 99US-0132137.
XX (UYNE-) UNIV NEW JERSEY MEDICINE & DENTISTRY.
XX Geller HM, Meiners S;
XX WPI; 2001-015974/02.
XX New peptides and methods of stimulating axonal and/or dendritic growth
XX and/or guidance by administering a peptide, particularly comprising a
XX tenascin-C region, to a neuron -
XX Disclosure; Page 20; 73pp; English.
XX The present invention relates to a tenascin-C peptide. The peptide,
XX particularly from a tenascin-C region, is used for stimulating axonal
XX and/or dendritic growth, independent of neurite guidance, and
XX stimulating axonal and/or dendritic guidance independent of axonal
XX and/or dendritic growth.
XX Sequence 798 AA;
SQ
Query Match 69.5%; Score 41; DB 22; Length 798;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 RLRSGEPQ 9
Db 122 RLRSGEPQ 129
RESULT 6
AAM41146
ID AAM41146 standard; Protein; 805 AA.
XX AAM41146;
DT 22-OCT-2001 (first entry)
DE Human polypeptide SEQ ID NO 6077.
XX Human; neurotropic; immunosuppressant; cytostatic; gene therapy; cancer;
XX peripheral nervous system; neuropathy; central nervous system; CNS;
XX Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
XX amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
XX chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
XX leukaemia.
XX Homo sapiens.
XX OS
XX WO200153312-A1.
XX 26-JUL-2001.
XX 26-DEC-2000; 2000WO-US34263.
XX 21-JAN-2000; 2000US-0488725.
XX 25-APR-2000; 2000US-0552317.
XX 09-JUL-2000; 2000US-0598042.
XX 19-JUL-2000; 2000US-0620312.
XX 03-AUG-2000; 2000US-0653450.
XX 14-SEP-2000; 2000US-0662191.
XX 19-OCT-2000; 2000US-0693036.
XX 29-NOV-2000; 2000US-0727344.
XX (HYSE-) HYSEQ INC.
PA

XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
XX Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
XX Zhao QA, Zhou P, Goodrich R, Drmanac RT;
XX WPI; 2001-442253/47.
XX N-PSDB; AAI60302.
XX Novel nucleic acids and polypeptides, useful for treating disorders
XX such as central nervous system injuries -
XX Example 2; SEQ ID NO 6077; 10078pp; English.
XX The invention relates to human nucleic acids (AAI57798-AAI61369) and
XX the encoded polypeptides (AAM38642-AAM42213) with neurotropic,
XX immunosuppressant and cytostatic activity. The polynucleotides are useful
XX in gene therapy. A composition containing a polypeptide or polynucleotide
XX of the invention may be used to treat diseases of the peripheral nervous
XX system, such as peripheral nervous injuries, peripheral neuropathy and
XX localised neuropathies and central nervous system diseases, such as
XX Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
XX lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
XX utilisation of the activities such as: immune system suppression,
XX Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
XX and thrombolytic activity; cancer diagnosis and therapy, drug screening,
XX assays for receptor activity, arthritis and inflammation, leukaemias and
XX C.N.S disorders.
XX Note: The sequence data for this patent did not form part of the printed
XX specification.
XX Sequence 805 AA;
SQ
Query Match 69.5%; Score 41; DB 22; Length 805;
Best Local Similarity 100.0%; Pred. No. 1.4e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 RLRSGEPQ 9
Db 126 RLRSGEPQ 133
RESULT 7
AAW70540
ID AAW70540 standard; Protein; 963 AA.
XX AAW70540;
XX 26-JAN-1999 (first entry)
XX Integrin beta-1 chain.
XX Integrin; beta-1 chain; immunoglobulin; chimeric; heterodimer complex;
XX inhibitor; binding; ligand; blood platelet; hemostatic; diagnostic agent;
XX human.
XX Homo sapiens.
XX OS
XX Key Location/Qualifiers
XX Peptide 1..20
XX Protein 21..963
XX /note= "signal peptide"
XX /note= "mature protein"
XX WO9832771-A1.
XX 30-JUL-1998.
XX 29-JAN-1998; 98WO-JP00370.
XX 29-AUG-1997; 97JP-0234544.
XX 29-JAN-1997; 97JP-0015118.
XX (TORA ) TORAY IND INC.
PA

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XX Kainoh M, Tanaka T;
 XX WPI; 1998-427881/36.
 DR N-PSDB; AAV33773.
 XX
 XX Integrin-immunoglobulin chimeric protein heterodimer complexes as
 PT platelet substitutes - contain the alpha and beta integrin chains
 PT associated in stable state and bind to extracellular matrix in the
 PT presence of plasma components
 XX
 XX Claim 9; Pages 50-57; 87pp; Japanese.
 XX
 CC This represents an integrin beta-1 chain. The invention provides
 CC integrin-immunoglobulin chimeric protein heterodimer complexes that
 CC comprise an integrin alpha or beta chain associated with an
 CC immunoglobulin light or heavy chain. These chimeric proteins form
 CC heterodimer complexes, in particular with a chimeric protein containing
 CC an integrin alpha chain and an immunoglobulin chain with a chimeric
 CC protein containing an integrin beta chain and an immunoglobulin chain;
 CC the immunoglobulin chain in each case may be a heavy chain, or one of the
 CC two may be a light chain. The integrin alpha chain is preferably alpha 4
 CC or alpha 2 and the integrin beta chain is preferably beta 1. Animal cells
 CC transformed with vectors containing the DNA coding for the above chimeric
 CC proteins can be used in the preparation of the chimeric proteins and
 CC their heterodimer complexes. The heterodimer complexes, which are useful
 CC for testing potential promoters and inhibitors of the binding of
 CC integrins to their ligands, function as blood platelet substitutes and
 CC hemostatics and as diagnostic agents.
 XX
 SQ Sequence 963 AA;
 Query Match 69.5%; Score 41; DB 19; Length 963;
 Best Local Similarity 100.0%; Pred. No. 1.6e-02;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 2 RLRSGEPPQ 9
 Db 122 RLRSGEPPQ 129
 |||||
 RESULT 8
 ABG29623
 ID ABG29623 standard; Protein; 62 AA.
 XX
 AC ABG29623;
 DT 18-FEB-2002 (first entry)
 XX
 DE Novel human diagnostic protein #29614.
 XX
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US08631.
 XX
 XX 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 XX
 XX (HYSE-) HYSEQ INC.
 PA
 XX Drmanac RT, Liu C, Tang YT;
 PI
 XX WPI; 2001-639362/73.
 DR N-PSDB; AAS93810.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in

PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -
 XX
 XX Claim 20; SEQ ID No 59982; 103pp; English.
 PS
 CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG0010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 XX
 SQ Sequence 62 AA;
 Query Match 67.8%; Score 40; DB 22; Length 62;
 Best Local Similarity 66.7%; Pred. No. 20;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 1 CRLRSGEPPQ 9
 Db 2 CRLRSAGDPR 10
 |||||
 RESULT 9
 ABG21707
 ID ABG21707 standard; Protein; 145 AA.
 XX
 AC ABG21707;
 XX
 DT 18-FEB-2002 (first entry)
 XX
 DE Novel human diagnostic protein #21698.
 XX
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200175067-A2.
 XX
 PD 11-OCT-2001.
 XX
 PF 30-MAR-2001; 2001WO-US08631.
 XX
 XX 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 XX
 XX (HYSE-) HYSEQ INC.
 PA
 XX Drmanac RT, Liu C, Tang YT;
 PI
 XX WPI; 2001-639362/73.
 DR N-PSDB; AAS85894.
 XX
 PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess

PT XX biodiversity -

PS Claim 20; SEQ ID No 52066; 103pp; English.

XX CC The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

CC at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 145 AA;

Query Match 67.8%; Score 40; DB 22; Length 145;

Best Local Similarity 70.0%; Pred. No. 43;

Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRLRSGEPOC 10

DB 96 CRARSGEEXC 105

RESULT 10

ABG21688

ID ABG21688 standard; Protein; 191 AA.

XX AC ABG21688;

XX DT 18-FEB-2002 (first entry)

XX DE Novel human diagnostic protein #21679.

XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;

KW food supplement; medical imaging; diagnostic; genetic disorder.

XX OS Homo sapiens.

XX PN WO200175067-A2.

XX PD 11-OCT-2001.

XX PF 30-MAR-2001; 2001WO-US08631.

XX PR 31-MAR-2000; 2000US-0540217.

PR 23-AUG-2000; 2000US-0549167.

XX PA (HYSE-) HYSEQ INC.

XX PI Drmanac RT, Liu C, Tang YT;

XX DR WPI; 2001-639362/73.

DR N-PSDB; AAS85875.

XX PT New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity -

PT biodiversity -

PS Claim 20; SEQ ID No 52047; 103pp; English.

XX CC The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic amino acid sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

CC at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 191 AA;

Query Match 67.8%; Score 40; DB 22; Length 191;

Best Local Similarity 70.0%; Pred. No. 55;

Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRLRSGEPOC 10

DB 78 CRARSGEEXC 87

RESULT 11

ABG21679

ID ABG21679 standard; Protein; 205 AA.

XX AC ABG21679;

XX DT 18-FEB-2002 (first entry)

XX DE Novel human diagnostic protein #21670.

XX KW Human; chromosome mapping; gene mapping; gene therapy; forensic;

KW food supplement; medical imaging; diagnostic; genetic disorder.

XX OS Homo sapiens.

XX PN WO200175067-A2.

XX PD 11-OCT-2001.

XX PF 30-MAR-2001; 2001WO-US08631.

XX PR 31-MAR-2000; 2000US-0540217.

PR 23-AUG-2000; 2000US-0649167.

XX PA (HYSE-) HYSEQ INC.

XX PI Drmanac RT, Liu C, Tang YT;

XX DR WPI; 2001-639362/73.

DR N-PSDB; AAS85866.

XX PT New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity -

PT biodiversity -

PS Claim 20; SEQ ID No 52038; 103pp; English.

CC The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 CC
 XX SQ Sequence 205 AA;

Query Match 67.8%; Score 40; DB 22; Length 205;
 Best Local Similarity 70.0%; Pred. No. 59;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRLRSGEQC 10
 II IIII I
 DB 128 CRARSGEEXC 137

RESULT 12
 ABG21676
 ID ABG21676 standard; Protein; 207 AA.

XX AC ABG21676;

DT 18-FEB-2002 (first entry)

DE Novel human diagnostic protein #21667.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.

XX OS Homo sapiens.

PN W0200175067-A2.

XX PD 11-OCT-2001.

XX PF 30-MAR-2001; 2001WO-US08631.

XX PR 31-MAR-2000; 2000US-0540217.

XX PR 23-AUG-2000; 2000US-0649167.

XX PA (HYSE-) HYSEQ INC.

XX PI Drmanac RT, Liu C, Tang YT;

XX DR WPI; 2001-639362/73.

XX DR N-PSDB; AAS85863.

XX PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.

XX PS Claim 20; SEQ ID NO 52035; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and

CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome

CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.
 CC
 XX SQ Sequence 207 AA;

Query Match 67.8%; Score 40; DB 22; Length 207;
 Best Local Similarity 70.0%; Pred. No. 59;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRLRSGEQC 10
 II IIII I
 DB 96 CRARSGEEXC 105

RESULT 13
 ABG21675
 ID ABG21675 standard; Protein; 247 AA.

XX AC ABG21675;

DT 18-FEB-2002 (first entry)

DE Novel human diagnostic protein #21666.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.

XX OS Homo sapiens.

PN W0200175067-A2.

XX PD 11-OCT-2001.

XX PF 30-MAR-2001; 2001WO-US08631.

XX PR 31-MAR-2000; 2000US-0540217.

XX PR 23-AUG-2000; 2000US-0649167.

XX PA (HYSE-) HYSEQ INC.

XX PI Drmanac RT, Liu C, Tang YT;

XX DR WPI; 2001-639362/73.

XX DR N-PSDB; AAS85862.

XX PT New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity.

XX PS Claim 20; SEQ ID NO 52034; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and

CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The

CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 247 AA;
 SQ Query Match 67.8%; Score 40; DB 22; Length 247;
 Best Local Similarity 70.0%; Pred. No. 69;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CRLRSGEQPC 10
 II IIII I
 Db 134 CRARSGEEXC 143

RESULT 14
 ABG21680
 ID ABG21680 standard; Protein; 257 AA.

AC ABG21680;

DT 18-FEB-2002 (first entry)

DE Novel human diagnostic protein #21671.

KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.

OS Homo sapiens.

PN WO200175067-A2.

PD 11-OCT-2001.

PF 30-MAR-2001; 2001WO-US08631.

PR 31-MAR-2000; 2000US-0540217.

PR 23-AUG-2000; 2000US-0649167.

XX (HYSE-) HYSEQ INC.

PI Drmanac RT, Liu C, Tang YT;

DR WPI: 2001-639362/73.

DR N-PSDB; AAS85867.

XX New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -

PS Claim 20; SEQ ID No 52039; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques

CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 257 AA;

Query Match 67.8%; Score 40; DB 22; Length 257;
 Best Local Similarity 70.0%; Pred. No. 72;
 Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CRLRSGEQPC 10
 II IIII I
 Db 144 CRARSGEEXC 153

RESULT 15
 ABG06467
 ID ABG06467 standard; Protein; 1043 AA.

AC ABG06467;

DT 13-FEB-2002 (first entry)

DE Novel human diagnostic protein #6458.

KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW food supplement; medical imaging; diagnostic; genetic disorder.

OS Homo sapiens.

PN WO200175067-A2.

PD 11-OCT-2001.

PF 30-MAR-2001; 2001WO-US08631.

PR 31-MAR-2000; 2000US-0540217.

PR 23-AUG-2000; 2000US-0649167.

XX (HYSE-) HYSEQ INC.

PI Drmanac RT, Liu C, Tang YT;

DR WPI: 2001-639362/73.

DR N-PSDB; AAS70654.

XX New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -

PS Claim 20; SEQ ID No 36826; 103pp; English.

XX The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or

CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (ii) and its binding partners are useful in medical
 CC imaging of sites expressing (ii). (i) and (ii) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG0010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 1043 AA;

Query Match 67.8%; Score 40; DB 22; Length 1043;

Best Local Similarity 70.0%; Pred. No. 2.6e+02;

Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRLRSGEQC 10

Db 1022 CRLHSGEKPC 1031

Search completed: January 30, 2003, 13:32:58
 Job time : 36 secs

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OM protein - protein search, using sw model

Run on: January 30, 2003, 13:32:01 ; Search time 15 seconds
(without alignments)
19.615 Million cell updates/sec

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Perfect score: 59
Sequence: 1 CRLRSGEPQC 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/PCRUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------------|
| 1 | 41 | 69.5 | 798 | 2 | US-07-728-215-30 |
| 2 | 41 | 69.5 | 798 | 4 | US-08-938-085A-30 |
| 3 | 39 | 66.1 | 179 | 1 | US-07-668-648-8 |
| 4 | 39 | 66.1 | 179 | 2 | US-08-429-998-8 |
| 5 | 39 | 66.1 | 179 | 2 | US-08-431-333-8 |
| 6 | 39 | 66.1 | 179 | 5 | PCR-US91-02321-8 |
| 7 | 38.5 | 65.3 | 150 | 2 | US-08-867-676-3 |
| 8 | 38.5 | 65.3 | 163 | 2 | US-08-867-676-1 |
| 9 | 38 | 64.4 | 477 | 2 | US-08-560-098A-51 |
| 10 | 38 | 64.4 | 560 | 2 | US-08-095-728B-6 |
| 11 | 38 | 64.4 | 560 | 5 | PCR-US92-02320A-6 |
| 12 | 38 | 64.4 | 797 | 2 | US-08-095-728B-2 |
| 13 | 38 | 64.4 | 797 | 5 | PCR-US92-02320A-2 |
| 14 | 37 | 62.7 | 71 | 2 | US-08-972-008-4 |
| 15 | 37 | 62.7 | 71 | 4 | US-09-267-409-4 |
| 16 | 37 | 62.7 | 263 | 2 | US-08-972-008-2 |
| 17 | 37 | 62.7 | 263 | 4 | US-09-141-027-2 |
| 18 | 37 | 62.7 | 263 | 4 | US-09-267-409-2 |
| 19 | 36 | 61.0 | 472 | 2 | US-08-272-255-10 |
| 20 | 36 | 61.0 | 472 | 3 | US-08-964-268-4 |
| 21 | 36 | 61.0 | 472 | 5 | PCR-US95-08565-10 |
| 22 | 34 | 57.6 | 558 | 4 | US-08-836-567-6 |
| 23 | 34 | 57.6 | 739 | 1 | US-07-618-946B-22 |
| 24 | 34 | 57.6 | 767 | 4 | US-08-836-567-8 |
| 25 | 34 | 57.6 | 814 | 1 | US-07-618-946B-23 |
| 26 | 33 | 55.9 | 50 | 1 | US-08-377-687-13 |
| 27 | 33 | 55.9 | 50 | 1 | US-08-377-687-22 |

| | | | | | | |
|----|----|------|------|---|------------------|-------------------|
| 28 | 33 | 55.9 | 50 | 2 | US-08-777-192-13 | Sequence 13, Appl |
| 29 | 33 | 55.9 | 50 | 2 | US-08-777-192-22 | Sequence 22, Appl |
| 30 | 33 | 55.9 | 50 | 4 | US-08-971-982-13 | Sequence 13, Appl |
| 31 | 33 | 55.9 | 50 | 4 | US-08-971-982-22 | Sequence 22, Appl |
| 32 | 33 | 55.9 | 327 | 4 | US-09-290-640-66 | Sequence 66, Appl |
| 33 | 33 | 55.9 | 802 | 4 | US-09-632-098-2 | Sequence 2, Appl |
| 34 | 33 | 55.9 | 902 | 1 | US-08-396-479B-6 | Sequence 6, Appl |
| 35 | 33 | 55.9 | 902 | 1 | US-08-818-823-6 | Sequence 6, Appl |
| 36 | 33 | 55.9 | 1219 | 4 | US-08-882-046-5 | Sequence 5, Appl |
| 37 | 33 | 55.9 | 3567 | 2 | US-07-642-734C-4 | Sequence 4, Appl |
| 38 | 33 | 55.9 | 3567 | 3 | US-08-439-009A-4 | Sequence 4, Appl |
| 39 | 33 | 55.9 | 5588 | 4 | US-09-036-987A-6 | Sequence 6, Appl |
| 40 | 33 | 55.9 | 5588 | 4 | US-09-370-700-6 | Sequence 6, Appl |
| 41 | 32 | 54.2 | 49 | 1 | US-08-304-051-1 | Sequence 1, Appl |
| 42 | 32 | 54.2 | 49 | 5 | PCR-US95-11445-1 | Sequence 1, Appl |
| 43 | 32 | 54.2 | 113 | 1 | US-07-668-648-10 | Sequence 10, Appl |
| 44 | 32 | 54.2 | 113 | 2 | US-08-429-998-10 | Sequence 10, Appl |
| 45 | 32 | 54.2 | 113 | 2 | US-08-431-333-10 | Sequence 10, Appl |

ALIGNMENTS

RESULT 1
US-07-728-215-30
; Sequence 30, Application US/07728215
; Patent No. 5962643
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Dean
; APPLICANT: Quaranta, Vito
; APPLICANT: Pytela, Robert
; TITLE OF INVENTION: A No. 5962643el Integrin Beta Subunit and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
; CITY: San Diego
; STATE: California
; COUNTRY: United States of America
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07728,215
; FILING DATE: 19910711
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P31 8717
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 798 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
US-07-728-215-30

Query Match 69.5%; Score 41; DB 2; Length 798;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 CRLRSGEPQ 9

DB 122 CRLRSGEPQ 129

```
RESULT 2
US-08-938-085A-30
; Sequence 30, Application US/08938085A
; Patent No. 6339148
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Dean
; APPLICANT: Quaranta, Vito
; APPLICANT: Pytela, Robert
; TITLE OF INVENTION: A No. 6339148el Integrin Beta Subunit and Uses
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/938,085A
; FILING DATE: 26-SEP-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/738,215
; FILING DATE: 11-JUL-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Parent, Annette S.
; REGISTRATION NUMBER: 42,058
; REFERENCE/DOCKET NUMBER: 023070-080210US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 798 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-938-085A-30

Query Match 69.5%; Score 41; DB 4; Length 798;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RLRSGEPO 9
Db 122 RLRSGEPO 129

RESULT 3
US-07-668-648-8
; Sequence 8, Application US/07668648
; Patent No. 5416192
; GENERAL INFORMATION:
; APPLICANT: Shoyab, Mohammed
; APPLICANT: Plowman, Gregory D.
; TITLE OF INVENTION: EPITHELINS: NOVEL CYSTEINE-RICH GROWTH
; TITLE OF INVENTION: MODULATING PROTEINS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
```

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COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/668,648
; FILING DATE: 19910819
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 5624-161-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)790-9090
; TELEFAX: (212) 869-9741
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 179 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-07-668-648-8

Query Match 66.1%; Score 39; DB 1; Length 179;
Best Local Similarity 70.0%; Pred. No. 12;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CRLRSGEPOC 10
Db 151 CRLKSGEWAC 160

RESULT 4
US-08-429-998-8
; Sequence 8, Application US/08429998
; Patent No. 5885961
; GENERAL INFORMATION:
; APPLICANT: Shoyab, Mohammed
; APPLICANT: Plowman, Gregory D.
; TITLE OF INVENTION: EPITHELINS: NOVEL CYSTEINE-RICH GROWTH
; TITLE OF INVENTION: MODULATING PROTEINS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/429,998
; FILING DATE: 27-APR-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/668,648
; FILING DATE: 13-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 5624-161-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)790-9090
; TELEFAX: (212) 869-9741
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 179 amino acids
; TYPE: amino acid
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
us-08-429-998-8

Query Match 66.1%; Score 39; DB 2; Length 179;
Best Local Similarity 70.0%; Pred. No. 12;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CRLRSGEQC 10
Db 151 CRLKSGEWAC 160

RESULT 5
US-08-431-333-8
; Sequence 8, Application US/08431333
; Patent No. 5965723
; GENERAL INFORMATION:
; APPLICANT: Shoyab, Mohammed
; APPLICANT: PLOWMAN, Gregory D.
; TITLE OF INVENTION: NOVEL CYSTEINE-RICH GROWTH
; TITLE OF INVENTION: MODULATING PROTEINS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/431,333
; FILING DATE: 27-APR-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION NUMBER: US 07/668,648
; FILING DATE: 13-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: MISROCK, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 5624-161-999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)790-9090
; TELEFAX: (212) 869-9741
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 179 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
us-08-431-333-8

Query Match 66.1%; Score 39; DB 2; Length 179;
Best Local Similarity 70.0%; Pred. No. 12;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CRLRSGEQC 10
Db 151 CRLKSGEWAC 160

RESULT 6
PCT-US91-02321-8
; Sequence 8, Application PC/TUS9102321
; GENERAL INFORMATION:
; APPLICANT: Shoyab, Mohammed
; APPLICANT: PLOWMAN, Gregory D.
; TITLE OF INVENTION: NOVEL CYSTEINE-RICH GROWTH
; TITLE OF INVENTION: EPITHELINS: NOVEL CYSTEINE-RICH GROWTH
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bristol-Myers Squibb Company
; STREET: 3005 First Avenue
; CITY: Seattle
; STATE: Washington
; COUNTRY: USA
; ZIP: 98121
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/02321
; FILING DATE: 19910403
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Poor, Brian W.
; REGISTRATION NUMBER: 32,928
; REFERENCE/DOCKET NUMBER: ON0071A-PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206)728-4800
; TELEFAX: (206)448-4775
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 179 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US91-02321-8

Query Match 66.1%; Score 39; DB 5; Length 179;
Best Local Similarity 70.0%; Pred. No. 12;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CRLRSGEQC 10
Db 151 CRLKSGEWAC 160

RESULT 7
US-08-867-676-3
; Sequence 3, Application US/08867676
; Patent No. 5866119
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Lal, Preeti
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: NEW HUMAN RIBONUCLEASE
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/867,676
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J J
```

REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0304 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 150 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: GenBank
CLONE: 1513102
US-08-867-676-3

Query Match 65.3%; Score 38.5; DB 2; Length 150;
Best Local Similarity 72.7%; Pred. No. 13;
Matches 8; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 CRLRSCE-PQC 10
||| ||: |||
DB 104 CRLTSGKYPQC 114

RESULT 8
US-08-867-676-1
; Sequence 1, Application US/08867676
; Patent No. 5866119
; GENERAL INFORMATION:
; APPLICANT: Bandman, Olga
; APPLICANT: Lal, Preeti
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: NEW HUMAN RIBONUCLEASE
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/867,676
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J J
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0304 US
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 163 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: SININOT01
; CLONE: 2181484
US-08-867-676-1

Query Match 65.3%; Score 38.5; DB 2; Length 163;
Best Local Similarity 72.7%; Pred. No. 14;
Matches 8; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 CRLRSCE-PQC 10
||| ||: |||
DB 104 CRLTSGKYPQC 114

RESULT 9
US-08-560-098A-51
; Sequence 51, Application US/08560098A
; Patent No. 5976841
; GENERAL INFORMATION:
; APPLICANT: WENNDT, Stephan
; APPLICANT: HEINZEL-WIELAND, Regina
; APPLICANT: STEFFENS, Gerd Josef
; TITLE OF INVENTION: Proteins having Fibrinolytic and
; TITLE OF INVENTION: Coagulation-inhibiting Properties
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, Mckown, Edwards & Lenahan
; STREET: 1200 G Street, N.W., Suite 700
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/560,098A
; FILING DATE: 17-NOV-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: P 44 40 892.7
; FILING DATE: 17-NOV-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: EVANS, Joseph D.
; REGISTRATION NUMBER: 26,269
; REFERENCE/DOCKET NUMBER: 148/42448
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-8800
; TELEFAX: (202) 628-8844
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 477 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-560-098A-51

Query Match 64.4%; Score 38; DB 2; Length 477;
Best Local Similarity 66.7%; Pred. No. 47;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 RLRSGEPC 10
||: || |||
DB 326 QLKSGSPQC 334

RESULT 10
US-08-095-728B-6
; Sequence 6, Application US/08095728B
; Patent No. 5843642
; GENERAL INFORMATION:
; APPLICANT: DMITROVSKY, ETHAN
; APPLICANT: WARRELL JR, RAYMOND P
; APPLICANT: MILLER JR, WILSON H
; APPLICANT: FRANKEL, STANLEY

```

; TITLE OF INVENTION: METHODS FOR THE DETECTION AND
; TITLE OF INVENTION: TREATMENT OF ACUTE PROMYELOCYTIC LEUKEMIA (APL)
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: COOPER & DUNHAM LLP
; STREET: 1185 AVENUE OF THE AMERICAS
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/095,728B
; FILING DATE: 21-JUL-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/673,838
; FILING DATE: 22-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: WHITE, JOHN P
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 38694-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 560 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-095-728B-6

Query Match 64.4% Score 38; DB 2; Length 560;
Best Local Similarity 77.8%; Pred. No. 55;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CRLRSGEPQ 9
Db 357 CRLRQEEPQ 365

RESULT 11
PCT-US92-02320A-6
; Sequence 6, Application PC/TUS9202320A
; GENERAL INFORMATION:
; APPLICANT: Sloan-Kettering Institute, For Cancer Research
; TITLE OF INVENTION: METHODS FOR DETECTION AND TREATMENT OF CANCER
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: COOPER & DUNHAM
; STREET: 30 ROCKEFELLER PLAZA
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/02320A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 675,084
; FILING DATE: 22-MAR-1991
; PRIOR APPLICATION DATA:

```

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; APPLICATION NUMBER: US 673,838
; FILING DATE: 22-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: WHITE, JOHN P
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 38694-PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 644-0525
; TELEX: (212) 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 560 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US92-02320A-6

Query Match 64.4% Score 38; DB 5; Length 560;
Best Local Similarity 77.8%; Pred. No. 55;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CRLRSGEPQ 9
Db 357 CRLRQEEPQ 365

RESULT 12
US-08-095-728B-2
; Sequence 2, Application US/08095728B
; Patent No. 5843642
; GENERAL INFORMATION:
; APPLICANT: DMITROVSKY, ETHAN
; APPLICANT: WARRELL JR, RAYMOND P
; APPLICANT: MILLER JR, WILSON H
; APPLICANT: FRANKEL, STANLEY
; TITLE OF INVENTION: METHODS FOR THE DETECTION AND
; TITLE OF INVENTION: TREATMENT OF ACUTE PROMYELOCYTIC LEUKEMIA (APL)
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: COOPER & DUNHAM LLP
; STREET: 1185 AVENUE OF THE AMERICAS
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/095,728B
; FILING DATE: 21-JUL-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/673,838
; FILING DATE: 22-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: WHITE, JOHN P
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 38694-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 278-0400
; TELEFAX: (212) 391-0525
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 797 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-095-728B-2

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Query Match 64.4%; Score 38; DB 2; Length 797;
Best Local Similarity 77.8%; Pred. No. 78;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CRLRSGEPQ 9
DB 357 CRLRQEEPQ 365

RESULT 13
PCT-US92-02320A-2
; Sequence 2, Application PC/TUS9202320A
; GENERAL INFORMATION:
; APPLICANT: Sloan-Kettering Institute, For Cancer Research
; TITLE OF INVENTION: METHODS FOR DETECTION AND TREATMENT OF CANCER
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: COOPER & DUNHAM
; STREET: 30 ROCKEFELLER PLAZA
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.24
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/02320A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA: US 675,084
; APPLICATION NUMBER: US 675,084
; FILING DATE: 22-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 673,838
; FILING DATE: 22-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: WHITE, JOHN P
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 38694-PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 644-0525
; TELEX: (212) 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 797 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US92-02320A-2

Query Match 64.4%; Score 38; DB 5; Length 797;
Best Local Similarity 77.8%; Pred. No. 78;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CRLRSGEPQ 9
DB 357 CRLRQEEPQ 365

RESULT 14
US-08-972-008-4
; Sequence 4, Application US/08972008
; Patent No. 5942420
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; TITLE OF INVENTION: No. 5942420el Molecules of the Follistatin-Related
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/267,409
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/972,008
; FILING DATE: 1997-NOV-17
; ATTORNEY/AGENT INFORMATION:
; NAME: Amy E. Mandragouras
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MEI-003DV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214

STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/972,008
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Amy E. Mandragouras
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MNI-026
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 71 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: Internal
US-08-972-008-4

Query Match 62.7%; Score 37; DB 2; Length 71;
Best Local Similarity 50.0%; Pred. No. 11;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRLRSGEPQ 10
DB 14 CRLMGRPRC 23

RESULT 15
US-09-267-409-4
; Sequence 4, Application US/09267409
; Patent No. 6410232
; GENERAL INFORMATION:
; APPLICANT: Holtzman, Douglas A.
; TITLE OF INVENTION: No. 6410232el Molecules of the Follistatin-Related
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/267,409
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/972,008
; FILING DATE: 1997-NOV-17
; ATTORNEY/AGENT INFORMATION:
; NAME: Amy E. Mandragouras
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: MEI-003DV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214

; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 71 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: internal
US-09-267-409-4

Query Match 62.7%; Score 37; DB 4; Length 71;
Best Local Similarity 50.0%; Pred. No. 11;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CRLRSGEPOC 10
||: ||:|
Db 14 CRMLGGRPRC 23

Search completed: January 30, 2003, 13:33:42
Job time : 16 secs

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OM protein - protein search, using sw model

Run on: January 30, 2003, 13:33:26 ; Search time 10 seconds
(without alignments)
20.179 Million cell updates/sec

Title: US-09-615-624A-1
Perfect score: 59
Sequence: 1 CRLRSGEPQC 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 122226 seqs, 20178551 residues

Total number of hits satisfying chosen parameters: 122226

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length | ID | Description |
|------------|-------|---------------|--------|----------------------|--------------------|
| 1 | 41 | 69.5 | 543 | 10 US-09-778-927A-67 | Sequence 67, Appl |
| 2 | 41 | 69.5 | 662 | 10 US-09-778-927A-66 | Sequence 66, Appl |
| 3 | 41 | 69.5 | 798 | 9 US-10-072-841-30 | Sequence 30, Appl |
| 4 | 41 | 69.5 | 798 | 12 US-10-100-912-6 | Sequence 6, Appl |
| 5 | 37 | 62.7 | 263 | 9 US-10-101-392-2 | Sequence 2, Appl |
| 6 | 37 | 62.7 | 263 | 9 US-10-066-500-41 | Sequence 41, Appl |
| 7 | 37 | 62.7 | 263 | 9 US-10-053-107-4 | Sequence 4, Appl |
| 8 | 37 | 62.7 | 263 | 9 US-10-028-072-484 | Sequence 484, Appl |
| 9 | 37 | 62.7 | 798 | 9 US-10-117-295A-1 | Sequence 1, Appl |
| 10 | 36 | 61.0 | 458 | 9 US-09-843-905A-15 | Sequence 15, Appl |
| 11 | 35 | 59.3 | 1798 | 10 US-09-938-275-9 | Sequence 9, Appl |
| 12 | 35 | 59.3 | 1798 | 10 US-09-845-583-8 | Sequence 8, Appl |
| 13 | 35 | 59.3 | 1799 | 10 US-09-845-583-6 | Sequence 6, Appl |
| 14 | 35 | 59.3 | 1801 | 10 US-09-938-275-8 | Sequence 8, Appl |
| 15 | 35 | 59.3 | 3635 | 10 US-09-845-583-2 | Sequence 2, Appl |
| 16 | 34 | 57.6 | 757 | 10 US-09-919-603-3 | Sequence 3, Appl |
| 17 | 33 | 55.9 | 50 | 10 US-09-759-584-13 | Sequence 13, Appl |
| 18 | 33 | 55.9 | 50 | 10 US-09-759-584-22 | Sequence 22, Appl |
| 19 | 33 | 55.9 | 204 | 10 US-09-948-018-18 | Sequence 18, Appl |

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|----|------|------|-----|------------------------|--------------------|
| 20 | 33 | 55.9 | 206 | 10 US-09-887-855-5 | Sequence 5, Appl |
| 21 | 33 | 55.9 | 268 | 10 US-09-815-242-11977 | Sequence 11977, A |
| 22 | 33 | 55.9 | 270 | 10 US-09-764-855-145 | Sequence 145, App |
| 23 | 33 | 55.9 | 327 | 10 US-09-802-669-66 | Sequence 66, Appl |
| 24 | 33 | 55.9 | 334 | 9 US-09-738-626-5849 | Sequence 5849, App |
| 25 | 33 | 55.9 | 372 | 9 US-10-028-072-106 | Sequence 106, App |
| 26 | 33 | 55.9 | 374 | 10 US-09-887-855-2 | Sequence 2, Appl |
| 27 | 32.5 | 55.1 | 273 | 10 US-09-764-864-1421 | Sequence 1421, App |
| 28 | 32.5 | 55.1 | 316 | 10 US-09-764-864-1036 | Sequence 1036, App |
| 29 | 32 | 54.2 | 44 | 10 US-09-925-299-1094 | Sequence 1094, App |
| 30 | 32 | 54.2 | 54 | 10 US-09-925-299-1361 | Sequence 1361, App |
| 31 | 32 | 54.2 | 61 | 10 US-09-925-299-1513 | Sequence 1513, App |
| 32 | 32 | 54.2 | 62 | 10 US-09-925-301-1475 | Sequence 1475, App |
| 33 | 32 | 54.2 | 68 | 10 US-09-764-855-95 | Sequence 95, Appl |
| 34 | 32 | 54.2 | 76 | 10 US-09-764-870-347 | Sequence 347, App |
| 35 | 32 | 54.2 | 76 | 10 US-09-764-853-548 | Sequence 548, App |
| 36 | 32 | 54.2 | 78 | 10 US-09-925-299-1091 | Sequence 1091, App |
| 37 | 32 | 54.2 | 80 | 10 US-09-925-301-1476 | Sequence 1476, App |
| 38 | 32 | 54.2 | 84 | 10 US-09-925-299-1518 | Sequence 1518, App |
| 39 | 32 | 54.2 | 89 | 10 US-09-925-297-646 | Sequence 646, App |
| 40 | 32 | 54.2 | 103 | 10 US-09-925-302-830 | Sequence 830, App |
| 41 | 32 | 54.2 | 104 | 10 US-09-764-855-111 | Sequence 111, App |
| 42 | 32 | 54.2 | 105 | 10 US-09-864-761-37162 | Sequence 37162, A |
| 43 | 32 | 54.2 | 113 | 10 US-09-925-301-1672 | Sequence 1672, App |
| 44 | 32 | 54.2 | 116 | 10 US-09-764-877-1993 | Sequence 1993, App |
| 45 | 32 | 54.2 | 119 | 10 US-09-925-297-867 | Sequence 867, App |

ALIGNMENTS

RESULT 1

US-09-778-927A-67
; Sequence 67, Application US/09778927A
; Patent No. US20020068342A1
; GENERAL INFORMATION:
; APPLICANT: KHOSRAVI, Rami et al.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID AND AMINO ACID SEQUENCES AND NOVEL
; FILE REFERENCE: VARIANTS OF ALTERNATIVE SPLICING
; CURRENT APPLICATION NUMBER: US/09/778,927A
; PRIOR FILING DATE: 2001-02-08
; PRIOR APPLICATION NUMBER: IL 134453
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: IL135341
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 67
; LENGTH: 543
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)-(543)
; OTHER INFORMATION: Xaa - any amino acid, unknown, or other
US-09-778-927A-67

Query Match 69.5%; Score 41; DB 10; Length 543;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RLRSGEPC 9

Db 122 RLRSGEPC 129

RESULT 2

US-09-778-927A-66
; Sequence 66, Application US/09778927A
; Patent No. US20020068342A1
; GENERAL INFORMATION:
; APPLICANT: KHOSRAVI, Rami et al.

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; TITLE OF INVENTION: NOVEL NUCLEIC ACID AND AMINO ACID SEQUENCES AND NOVEL
; FILE REFERENCE: 2786-0160P
; CURRENT APPLICATION NUMBER: US/09/778, 927A
; CURRENT FILING DATE: 2001-02-08
; PRIOR APPLICATION NUMBER: IL 134453
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: IL135341
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 66
; LENGTH: 662
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(662)
; OTHER INFORMATION: Xaa = any amino acid, unknown, or other
US-09-778-927A-66

Query Match          69.5%; Score 41; DB 10; Length 662;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 RLRSGEPQ 9
Db      122 RLRSGEPQ 129

RESULT 3
US-10-072-841-30
; Sequence 30, Application US/10072841
; Patent No. US20020164708A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Dean
; Pytela, Robert
; TITLE OF INVENTION: A No. US20020164708A1e1 Integrin Beta Subunit and Uses
; THEREOF
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States of America
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/072,841
; FILING DATE: 06-Feb-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/728,215
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P31 8717
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 798 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
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; SEQUENCE DESCRIPTION: SEQ ID NO: 30:
US-10-072-841-30

Query Match          69.5%; Score 41; DB 9; Length 798;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 RLRSGEPQ 9
Db      122 RLRSGEPQ 129

RESULT 4
US-10-100-912-6
; Sequence 6, Application US/10100912
; Patent No. US20020137459A1
; GENERAL INFORMATION:
; APPLICANT: Geller, Herbert M.
; APPLICANT: Meiners, Sally
; TITLE OF INVENTION: Neurite Outgrowth and Guidance by Tenascin-C
; FILE REFERENCE: 601-1-094
; CURRENT APPLICATION NUMBER: US/10/100,912
; CURRENT FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: PCT/US00/11647
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/132,137
; PRIOR FILING DATE: 1999-05-01
; NUMBER OF SEQ ID NOS: 12
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; SEQ ID NO 6
; LENGTH: 798
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-100-912-6

Query Match          69.5%; Score 41; DB 12; Length 798;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 RLRSGEPQ 9
Db      122 RLRSGEPQ 129

RESULT 5
US-10-101-392-2
; Sequence 2, Application US/10101392
; Patent No. US20020164714A1
; GENERAL INFORMATION:
; APPLICANT: Duan, et al.
; TITLE OF INVENTION: Follistatin-3
; FILE REFERENCE: PF388
; CURRENT APPLICATION NUMBER: US/10/101,392
; CURRENT FILING DATE: 2002-03-20
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/141,027
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-27
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/656,248
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-29
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 263
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-101-392-2

Query Match          62.7%; Score 37; DB 9; Length 263;
Best Local Similarity 50.0%; Pred. No. 27;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      1 CRLRSGEPC 10
Db      110 CRLGGRPC 119
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RESULT 6
US-10-066-500-41
; Sequence 41, Application US/10066500
; Patent No. US20020177169A1
; GENERAL INFORMATION:
; APPLICANT: Avi J. Ashkenazi
; APPLICANT: Kevin P. Baker
; APPLICANT: David A. Botstein
; APPLICANT: Luc Desnoyers
; APPLICANT: Dan L. Eaton
; APPLICANT: Napoleone Ferrara
; APPLICANT: Sherman Fong
; APPLICANT: Wei-Qiang Gao
; APPLICANT: Hanspeter Gerber
; APPLICANT: Mary E. Gerritsen
; APPLICANT: Audrey Goddard
; APPLICANT: Paul J. Godowski
; APPLICANT: Austin L. Gurney
; APPLICANT: Ivar J. Kljavin
; APPLICANT: Jennie P. Mather
; APPLICANT: Mary A. Napier
; APPLICANT: James Pan
; APPLICANT: Nicholas F. Paoni
; APPLICANT: Margaret Ann Roy
; APPLICANT: Timothy A. Stewart
; APPLICANT: Daniel Tumas
; APPLICANT: Colin K. Watanabe
; APPLICANT: P. Mickey Williams
; APPLICANT: William I. Wood
; APPLICANT: Zemin Zang
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3130R1C7
; CURRENT APPLICATION NUMBER: US/10/066,500
; CURRENT FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 10/002,796
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/056974
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/059115
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
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; PRIOR APPLICATION NUMBER: 60/063082
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; PRIOR FILING DATE: 1997-08-26
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; PRIOR FILING DATE: 1998-12-08
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; PRIOR APPLICATION NUMBER: 09/380139
; PRIOR FILING DATE: 1999-08-25
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; PRIOR FILING DATE: 1999-10-18
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; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: 09/808689
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; PRIOR FILING DATE: 2001-06-19
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; PRIOR APPLICATION NUMBER: PCT/US98/18824
; PRIOR FILING DATE: 1998-09-10
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; PRIOR APPLICATION NUMBER: PCT/US99/12252
; PRIOR FILING DATE: 1999-06-02
; PRIOR APPLICATION NUMBER: PCT/US99/20111
; PRIOR FILING DATE: 1999-09-01
; PRIOR APPLICATION NUMBER: PCT/US99/20594
; PRIOR FILING DATE: 1999-09-08
; PRIOR APPLICATION NUMBER: PCT/US99/21090
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: PCT/US99/21547

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Query Match 62.7%; Score 37; DB 9; Length 263;
Best Local Similarity 50.0%; Pred. No. 27;
Matches 5; Conservative 2; Mismatches 3; Indels 3; Gaps 0;

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DB 110 CRLMGRPRC 119

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RESULT 7
US-10-053-107-4
; Sequence 4, Application US/10053107
; Publication No. US20020192752A1
; GENERAL INFORMATION:

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; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Compositions and Methods for the Treatment of Immune
; FILE REFERENCE: P3033R1C1
; CURRENT APPLICATION NUMBER: US/10/053,107
; CURRENT FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: 60/099601
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/107783
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; PRIOR APPLICATION NUMBER: 60/108802
; PRIOR FILING DATE: 1998-11-17
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; PRIOR APPLICATION NUMBER: PCT/US01/21735
; PRIOR FILING DATE: 2001-07-09
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; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-053-107-4

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Query Match 62.7%; Score 37; DB 9; Length 263;
Best Local Similarity 50.0%; Pred. No. 27;
Matches 5; Conservative 2; Mismatches 3; Indels 3; Gaps 0;
OY 1 CRLRSGEPOC 10

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Db 110 CRLMGRPRC 119

RESULT 8

US-10-028-072-484
Sequence 484, Application US/10028072
Publication No. US20030004311A1

GENERAL INFORMATION:

APPLICANT: Baker, Kevin P.
APPLICANT: Beresini, Maureen
APPLICANT: DeForge, Laura
APPLICANT: Desnoyers, Luc
APPLICANT: Filvaroff, Ellen
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K
APPLICANT: Wood, William
APPLICANT: Zhang

TITLE OF INVENTION:

FILE REFERENCE:

CURRENT APPLICATION NUMBER: US/10/028,072

CURRENT FILING DATE: 2001-12-19

PRIOR APPLICATION NUMBER: 60/049911

PRIOR FILING DATE: 1997-06-18

PRIOR APPLICATION NUMBER: 60/056974

PRIOR FILING DATE: 1997-08-26

PRIOR APPLICATION NUMBER: 60/059113

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/059115

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/059117

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/059122

PRIOR FILING DATE: 1997-09-17

PRIOR APPLICATION NUMBER: 60/059184

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PRIOR APPLICATION NUMBER: 60/059263

PRIOR FILING DATE: 1997-09-18

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PRIOR FILING DATE: 1997-09-19

PRIOR APPLICATION NUMBER: 60/059588

PRIOR FILING DATE: 1997-09-19

PRIOR APPLICATION NUMBER: 60/059836

PRIOR FILING DATE: 1997-09-24

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PRIOR FILING DATE: 1997-10-31

PRIOR APPLICATION NUMBER: 60/063127

PRIOR FILING DATE: 1997-10-24

PRIOR APPLICATION NUMBER: 60/063327

PRIOR FILING DATE: 1997-10-27

PRIOR APPLICATION NUMBER: 60/063329

PRIOR FILING DATE: 1997-10-27

PRIOR APPLICATION NUMBER: 60/063550

PRIOR FILING DATE: 1997-10-28

PRIOR APPLICATION NUMBER: 60/063561
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PRIOR FILING DATE: 1997-11-03
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PRIOR FILING DATE: 1997-12-16
PRIOR APPLICATION NUMBER: 60/072320
PRIOR FILING DATE: 1998-01-23
PRIOR APPLICATION NUMBER: 60/073612
PRIOR FILING DATE: 1998-02-04
PRIOR APPLICATION NUMBER: 60/074086
PRIOR FILING DATE: 1998-02-09
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PRIOR FILING DATE: 1998-02-09
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/078910
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PRIOR APPLICATION NUMBER: 60/079294
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PRIOR APPLICATION NUMBER: 60/079663
PRIOR FILING DATE: 1998-02-27
PRIOR APPLICATION NUMBER: 60/079728
PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/080165
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/081203
PRIOR FILING DATE: 1998-04-09
PRIOR APPLICATION NUMBER: 60/081229
PRIOR FILING DATE: 1998-04-09
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PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081818
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/082999
PRIOR FILING DATE: 1998-04-24
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/083545
PRIOR FILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/084600

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; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084627
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084637
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/085149
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: 60/085323
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; PRIOR FILING DATE: 1998-05-28
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; PRIOR APPLICATION NUMBER: 60/088730
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; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088810
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088858
; PRIOR FILING DATE: 19/98-06-11
; PRIOR APPLICATION NUMBER: 60/089522
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089599
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; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/089947
; PRIOR FILING DATE: 1998-06-19
; PRIOR APPLICATION NUMBER: 60/090349
; PRIOR FILING DATE: 1998-06-23
; PRIOR APPLICATION NUMBER: 60/090429
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090445
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090538
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090863
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: 60/091360
; PRIOR FILING DATE: 1998-07-01
; PRIOR APPLICATION NUMBER: 60/091519
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07

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Query Match      62.7%; Score 37; DB 9; Length 263;
Best Local Similarity 50.0%; Pred. No. 27;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

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QY 1 CLRSRGEPC 10
    ||: ||:|
Db 110 CRMLGRRPC 119

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RESULT 9
US-10-117-295A-1
; Sequence 1, Application US/10117295A
; Publication No. US20020182678A1

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; GENERAL INFORMATION:
; APPLICANT: GARRIDO PAVON, Juan Jose
; APPLICANT: LLANES RUIZ, Diego
; APPLICANT: BABANCHO MEDINA, Manuel
; APPLICANT: JIMENEZ MARIN, Angeles Maria
; TITLE OF INVENTION: CD29 PIG PROTEIN, NUCLEIC ACID CODING FOR SAID PROTEIN
; FILE REFERENCE: 9256-13US
; CURRENT APPLICATION NUMBER: US/10/117,295A
; PRIOR FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: PCT/ES00/00374
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: P9902193
; PRIOR FILING DATE: 1999-10-05
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn version 2.0
; SEQ ID NO 1
; LENGTH: 798
; TYPE: PRT
; ORGANISM: Pig
US-10-117-295A-1

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Query Match      62.7%; Score 37; DB 9; Length 798;
Best Local Similarity 87.5%; Pred. No. 76;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 2 RLRSGEPC 9
    |||||
Db 122 QLRSGEPQ 129

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RESULT 10
US-09-843-905A-15
; Sequence 15, Application US/09843905A
; Patent No. US20020168683A1
; GENERAL INFORMATION:
; APPLICANT: Bird, Timothy A.
; TITLE OF INVENTION: HUMAN PELLINO POLYPEPTIDES
; FILE REFERENCE: 2990-A
; CURRENT APPLICATION NUMBER: US/09/843,905A
; CURRENT FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 60/200,198
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 458
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-09-843-905A-15

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Query Match      61.0%; Score 36; DB 9; Length 458;
Best Local Similarity 66.7%; Pred. No. 66;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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QY 2 RLRSGEPC 10
    ||: ||:|
Db 302 RLRSRGPQ 310

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RESULT 11
US-09-938-275-9
; Sequence 9, Application US/09938275
; Patent No. US2002011309A1
; GENERAL INFORMATION:
; APPLICANT: Gerardo Castillo
; APPLICANT: Alan Snow
; TITLE OF INVENTION: Therapeutic and Diagnostic Applications
; TITLE OF INVENTION: Of Laminin and Laminin-Derived Protein Fragments
; FILE REFERENCE: PROTEO.P03
; CURRENT APPLICATION NUMBER: US/09/938,275
; CURRENT FILING DATE: 2001-08-16

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; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 1798
; TYPE: PRT
; ORGANISM: Homo Sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Swissprot P55268
; DATABASE ENTRY DATE: 1996-10-01
US-09-938-275-9

Query Match      59.3%; Score 35; DB 10; Length 1798;
Best Local Similarity 50.0%; Pred. No. 3.5e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRLRSGEQPC 10
Db 1428 CRDEGQPC 1437

RESULT 12
US-09-845-583-8
; Sequence 8, Application US/09845583
; Patent No. US20020142954A1
; GENERAL INFORMATION:
; APPLICANT: Burgeson, Robert
; APPLICANT: Brunken, William Joseph
; APPLICANT: Champlaud, Marie-France
; APPLICANT: Hunter, Dale
; TITLE OF INVENTION: LAMININ 15 AND USES THEREOF
; FILE REFERENCE: 10287-056001
; CURRENT APPLICATION NUMBER: US/09/845,583
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: US 60/200,863
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 1798
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-845-583-8

Query Match      59.3%; Score 35; DB 10; Length 1798;
Best Local Similarity 50.0%; Pred. No. 3.5e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRLRSGEQPC 10
Db 1428 CRDEGQPC 1437

RESULT 13
US-09-845-583-6
; Sequence 6, Application US/09845583
; Patent No. US20020142954A1
; GENERAL INFORMATION:
; APPLICANT: Burgeson, Robert
; APPLICANT: Brunken, William Joseph
; APPLICANT: Champlaud, Marie-France
; APPLICANT: Hunter, Dale
; TITLE OF INVENTION: LAMININ 15 AND USES THEREOF
; FILE REFERENCE: 10287-056001
; CURRENT APPLICATION NUMBER: US/09/845,583
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: US 60/200,863
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 1799
; TYPE: PRT
; ORGANISM: Mus musculus

US-09-845-583-6

Query Match      59.3%; Score 35; DB 10; Length 1799;
Best Local Similarity 50.0%; Pred. No. 3.5e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRLRSGEQPC 10
Db 1429 CRDEGQPC 1438

RESULT 14
US-09-938-275-8
; Sequence 8, Application US/09938275
; Patent No. US2002011309A1
; GENERAL INFORMATION:
; APPLICANT: Gerardo Castillo
; APPLICANT: Alan Snow
; TITLE OF INVENTION: Therapeutic and Diagnostic Applications
; TITLE OF INVENTION: of Laminin and Laminin-Derived Protein Fragments
; FILE REFERENCE: PROTEO.P03
; CURRENT APPLICATION NUMBER: US/09/938,275
; CURRENT FILING DATE: 2001-08-16
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 1801
; TYPE: PRT
; ORGANISM: Rattus No. US2002011309A1vegicus
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Swissprot P15800
; DATABASE ENTRY DATE: 1990-04-01
US-09-938-275-8

Query Match      59.3%; Score 35; DB 10; Length 1801;
Best Local Similarity 50.0%; Pred. No. 3.5e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRLRSGEQPC 10
Db 1431 CRDEGQPC 1440

RESULT 15
US-09-845-583-2
; Sequence 2, Application US/09845583
; Patent No. US20020142954A1
; GENERAL INFORMATION:
; APPLICANT: Burgeson, Robert
; APPLICANT: Brunken, William Joseph
; APPLICANT: Champlaud, Marie-France
; APPLICANT: Hunter, Dale
; TITLE OF INVENTION: LAMININ 15 AND USES THEREOF
; FILE REFERENCE: 10287-056001
; CURRENT APPLICATION NUMBER: US/09/845,583
; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: US 60/200,863
; PRIOR FILING DATE: 2000-05-01
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 3635
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-845-583-2

Query Match      59.3%; Score 35; DB 10; Length 3635;
Best Local Similarity 60.0%; Pred. No. 6.9e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRLRSGEQPC 10
Db 1847 CVLRNGRTQC 1856

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Search completed: January 30, 2003, 13:37:27
Job time : 11 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 30, 2003, 13:32:01 ; Search time 15 seconds
(without alignments)
64.090 Million cell updates/sec

Title: US-09-615-624A-1
Perfect score: 59
Sequence: 1 CRLRSGEPQC 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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|------------|-------|-------------|--------|----------|--------------------|
| 1 | 45 | 76.3 | 3051 | 2 S42373 | hypothetical prote |
| 2 | 41 | 69.5 | 798 | 2 B27079 | fibronectin recept |
| 3 | 40 | 67.8 | 892 | 2 T15195 | hypothetical prote |
| 4 | 38.5 | 65.3 | 150 | 2 S72361 | pancreatic ribonuc |
| 5 | 38 | 64.4 | 394 | 2 JS0600 | t-plasminogen acti |
| 6 | 38 | 64.4 | 431 | 2 JS0599 | t-plasminogen acti |
| 7 | 38 | 64.4 | 477 | 1 A34369 | t-plasminogen acti |
| 8 | 38 | 64.4 | 477 | 2 JS0598 | t-plasminogen acti |
| 9 | 38 | 64.4 | 560 | 2 A60198 | PML-l protein - hu |
| 10 | 38 | 64.4 | 589 | 2 S42517 | PML protein, splic |
| 11 | 38 | 64.4 | 589 | 2 S44381 | PML protein, splic |
| 12 | 38 | 64.4 | 593 | 2 B40045 | probable transcrip |
| 13 | 38 | 64.4 | 633 | 2 S19244 | gene Myl protein - |
| 14 | 38 | 64.4 | 634 | 2 AG0252 | probable DEAD box |
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| 16 | 38 | 64.4 | 636 | 2 A85792 | probable enzyme 22 |
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| 18 | 38 | 64.4 | 636 | 2 H64941 | Probable ATP-depen |
| 19 | 38 | 64.4 | 641 | 2 A40045 | probable transcrip |
| 20 | 38 | 64.4 | 646 | 2 E82133 | ATP-dependent heli |
| 21 | 38 | 64.4 | 708 | 2 S01659 | integrin beta-1 ch |
| 22 | 38 | 64.4 | 799 | 1 LUNSF8 | fibronectin recept |
| 23 | 38 | 64.4 | 799 | 2 JC4126 | integrin beta olig |
| 24 | 38 | 64.4 | 802 | 2 S42518 | PML protein, splic |
| 25 | 38 | 64.4 | 802 | 2 S44382 | PML protein, splic |
| 26 | 38 | 64.4 | 860 | 2 S42516 | PML protein, splic |
| 27 | 38 | 64.4 | 860 | 2 S44380 | PML protein, splic |
| 28 | 38 | 64.4 | 860 | 2 S44380 | probable transcrip |
| 29 | 38 | 64.4 | 955 | 4 C40045 | |

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| 30 | 37 | 62.7 | 64 | 2 | T16954 | hypothetical prote |
| 31 | 37 | 62.7 | 161 | 2 | E71078 | hypothetical prote |
| 32 | 37 | 62.7 | 393 | 2 | T16046 | hypothetical prote |
| 33 | 37 | 62.7 | 484 | 2 | T25731 | hypothetical prote |
| 34 | 37 | 62.7 | 773 | 2 | I46059 | beta-1 integrin su |
| 35 | 36 | 61.0 | 151 | 2 | E69077 | hypothetical prote |
| 36 | 36 | 61.0 | 354 | 2 | T22274 | hypothetical prote |
| 37 | 36 | 61.0 | 405 | 2 | A82130 | transcription regu |
| 38 | 36 | 61.0 | 472 | 1 | W2ECD | deoxyribodipyrimid |
| 39 | 36 | 61.0 | 472 | 2 | E90720 | deoxyribodipyrimid |
| 40 | 36 | 61.0 | 472 | 2 | C85571 | hypothetical prote |
| 41 | 36 | 61.0 | 564 | 1 | VHXPMV | major structural n |
| 42 | 36 | 61.0 | 798 | 2 | A28193 | integrin beta-1 ch |
| 43 | 36 | 61.0 | 798 | 2 | B28193 | integrin beta-1* c |
| 44 | 36 | 61.0 | 2767 | 1 | UIHU | thyroglobulin prec |
| 45 | 35 | 59.3 | 121 | 2 | JX0279 | ribonuclease CL2 - |

ALIGNMENTS

RESULT 1

S42373
hypothetical protein T20G5.3 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 07-Oct-1994 #sequence_revision 10-Nov-1995 #text_change 16-Jul-1999
C:Accession: S42373
R:Smith, A.
submitted to the EMBL Data Library, March 1994
A:Reference number: S42368
A:Accession: S42373
A:Molecule type: DNA
A:Residues: 1-3051 <SMI>
A:Cross-references: EMBL:Z30423; NID:g458479; PID:g458485
C:Genetics:
A:Introns: 96/1; 166/3; 201/2; 355/1; 404/1; 427/2; 794/1; 892/1; 952/2; 1041/1; 1146
C:Superfamily: von Willebrand factor type A repeat homology; EGF homology; fibronectin
F;512-679/Domain: von Willebrand factor type A repeat homology <VWAL>
F;754-793/Domain: fibronectin type II repeat homology <2FI>
F;1201-1244/Domain: EGF homology <EGF>

Query Match 76.3%; Score 45; DB 2; Length 3051;
Best Local Similarity 70.0%; Pred. No. 12;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CRLRSGEPQC 10

Db 1372 CRLMGGEPC 1381
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RESULT 2

B27079
fibronectin receptor beta chain precursor - human
N:Alternate names: CD29 antigen; integrin beta-1 chain
C:Species: Homo sapiens (man)
C:Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 20-Aug-1999
C:Accession: B27079
R:Argaves, W.S.; Suzuki, S.; Arai, H.; Thompson, K.; Pierschbacher, M.D.; Ruoslahti, J.
J. Cell Biol. 105, 1183-1190, 1987
A:Title: Amino acid sequence of the human fibronectin receptor.
A:Reference number: A27079; MUID:88007843; PMID:2958481
A:Accession: B27079
A:Molecule type: mRNA
A:Residues: 1-798 <ARG>
A:Cross-references: EMBL:X07979; NID:g31441; PIDN:CAA30790.1; PID:g31442
C:Genetics:
A:Gene: GDB:ITGB1; FNRB
A:Cross-references: GDB:118732; OMIM:135630
A:Map position: 10p11.2-10p11.2
C:Superfamily: integrin beta chain; laminin-type EGF-like homology
C:Keywords: alternative splicing; duplication; heterodimer; transmembrane protein
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-798/Product: fibronectin receptor beta chain #status predicted <MAT>

Query Match 69.5%; Score 41; DB 2; Length 798;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RLRSGEPOC 9
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 Db 122 RLRSGEPOC 129

RESULT 3
 T15195
 Hypothetical protein F55A12.1 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
 C:Accession: T15195
 R:Pauley, A.; Gattung, S.
 Submitted to the EMBL Data Library, May 1997
 A:Description: The sequence of C. elegans cosmid F55A12.
 A:Reference number: T18305
 A:Accession: T15195
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-892 <PAU>
 A:Cross-references: EMBL:AF003130; NID:g2088663; PID:g2088671; PIDN:AAB54129.1; GSPDB:GN
 A:Experimental source: strain Bristol N2; clone F55A12
 C:Genetics:
 A:Gene: CESP:F55A12.1
 A:Map position: 1
 A:Introns: 55/3; 75/3; 216/2; 460/3; 517/3; 558/1; 673/3; 753/3; 856/2

Query Match 67.8%; Score 40; DB 2; Length 892;
 Best Local Similarity 60.0%; Pred. No. 31;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRLRSGEPOC 10
 |||||
 Db 511 CRFSSGDPPC 520

RESULT 4
 S72361
 pancreatic ribonuclease (EC 3.1.27.5) k6 precursor - human
 N:Alternate names: RNase K6
 C:Species: Homo sapiens (man)
 C:Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 08-May-1998
 C:Accession: S72361; S72362
 R:Rosenberg, H.F.; Dyer, K.D.
 submitted to the EMBL Data Library, July 1996
 A:Description: Molecular cloning and characterization of a novel human ribonuclease (RNA
 A:Reference number: S72361
 A:Accession: S72361
 A:Molecule type: DNA
 A:Residues: 1-150 <NOS>
 A:Cross-references: EMBL:U64998; NID:g1513101; PID:g1513102
 R:Rosenberg, H.F.; Dyer, K.D.
 Nucleic Acids Res. 24, 3507-3513, 1996
 A:Title: Molecular cloning and characterization of a novel human ribonuclease (RNase k6)
 A:Reference number: S72362; MUID:96433147; PMID:8836175
 A:Accession: S72362
 A:Status: nucleic acid sequence not shown
 A:Molecule type: DNA
 A:Residues: 24-150 <ROW>
 A:Cross-references: EMBL:U64998
 C:Genetics:
 A:Map position: 14
 C:Superfamily: pancreatic ribonuclease
 C:Keywords: glycoprotein; hydrolase; nucleic acid degradation
 F:1-23/Domain: signal sequence #status predicted <SIG>
 F:24-150/Product: pancreatic ribonuclease #status predicted <MAT>
 F:46-104/60-114/78-129; 85-92/Disulfide bonds: #status predicted
 F:55,100/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 65.3%; Score 38.5; DB 2; Length 150;
 Best Local Similarity 72.7%; Pred. No. 11;
 Matches 8; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 CRLRSGE-POC 10
 |||||
 Db 104 CRLTSGKYPQC 114

RESULT 5
 JS0600
 t-plasminogen activator (EC 3.4.21.68) gamma precursor - common vampire bat
 N:Alternate names: tissue plasminogen activator
 C:Species: Desmodus rotundus (common vampire bat)
 C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jul-1999
 C:Accession: JS0600
 R:Kraetzschmar, J.; Haendler, B.; Langer, G.; Boidol, W.; Bringmann, P.; Alagon, A.;
 Gene 105, 229-237, 1991
 A:Title: The plasminogen activator family from the salivary gland of the vampire bat
 A:Reference number: JS0597; MUID:92039036; PMID:1937019
 A:Accession: JS0600
 A:Molecule type: mRNA
 A:Residues: 1-394 <KRA>
 A:Cross-references: GB:M63990; NID:g166078; PIDN:AAA31595.1; PID:g166079
 A:Note: The authors translated the codon ATC for residue 75 as Thr
 C:Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I repeat
 C:Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase
 F:1-21/Domain: signal sequence #status predicted <SIG>
 F:22-36/Domain: propeptide #status predicted <PRO>
 F:37-394/Product: plasminogen activator gamma #status predicted <PLA>
 F:45-126/Domain: kringle homology <KRG>
 F:143-388/Domain: trypsin homology <TRY>
 F:45-126,66-108,97-121,131-262,174-190,182-251,276-351,308-324,341-369/Disulfide bond
 F:142-143/Cleavage site: His-Ser (plasma) #status predicted
 F:189,238,345/Active site: His, Asp, Ser #status predicted
 F:315/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 64.4%; Score 38; DB 2; Length 394;
 Best Local Similarity 66.7%; Pred. No. 34;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 RLRSGEPOC 10
 |||||
 Db 243 QLKSGSPQC 251

RESULT 6
 JS0599
 t-plasminogen activator (EC 3.4.21.68) beta precursor - common vampire bat
 N:Alternate names: tissue plasminogen activator
 C:Species: Desmodus rotundus (common vampire bat)
 C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jul-1999
 C:Accession: JS0599
 R:Kraetzschmar, J.; Haendler, B.; Langer, G.; Boidol, W.; Bringmann, P.; Alagon, A.;
 Gene 105, 229-237, 1991
 A:Title: The plasminogen activator family from the salivary gland of the vampire bat
 A:Reference number: JS0597; MUID:92039036; PMID:1937019
 A:Accession: JS0599
 A:Molecule type: mRNA
 A:Residues: 1-431 <KRA>
 A:Cross-references: GB:M63989; NID:g166076; PIDN:AAA31594.1; PID:g166077
 C:Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I repeat
 C:Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase
 F:1-21/Domain: signal sequence #status predicted <SIG>
 F:22-36/Domain: propeptide #status predicted <PRO>
 F:37-431/Product: plasminogen activator beta #status predicted <PLA>
 F:41-74/Domain: EGF homology <EGF>
 F:82-163/Domain: kringle homology <KRG>
 F:180-425/Domain: trypsin homology <TRY>
 F:41-52,46-63,65-74,82-163,103-145,134-158,168-299,211-227,219-288,313-388/Disulfide
 F:139,352/Binding site: carbohydrate (Asn) (covalent) #status predicted
 F:179-180/Cleavage site: His-Ser (plasma) #status predicted
 F:226,275,382/Active site: His, Asp, Ser #status predicted

F:345-361,378-406/Disulfide bonds: #status predicted

Query Match 64.4%; Score 38; DB 2; Length 431;
Best Local Similarity 66.7%; Pred. No. 36;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 RLRSGEPC 10
:||| |||

Db 280 QLKSGSPQC 288

RESULT 7

A34369
t-plasminogen activator (EC 3.4.21.68) precursor - false vampire bat (Megaderma lyra)
C:Species: Megaderma lyra
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A34369
R:Gardell, S.J.; Duong, L.T.; Diehl, R.E.; York, J.D.; Hare, T.R.; Register, R.B.; Jacob
J. Biol. Chem. 264, 17947-17952, 1989
A:Title: Isolation, characterization, and cDNA cloning of a vampire bat salivary plasmin
A:Reference number: A34369; MUID:90036867; PMID:2509450
A:Accession: A34369
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-477 <GAR>
A:Cross-references: GB:J05082; NID:gl66080; PIDN:AAA31596.1; PID:gl66081
C:Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I repeat hom
C:Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-36/Domain: propeptide #status predicted <PRO>
F:37-477/Product: plasminogen activator #status predicted <PLA>
F:42-79/Domain: fibronectin type I repeat homology <IFR>
F:87-120/Domain: EGF homology <EGF>
F:128-209/Domain: kringle homology <KR>
F:226-471/Domain: trypsin homology <TRY>
F:42-72,70-79,87-98,92-109,111-120,128-209,149-191,180-204,214-345,257-273,265-334,359-4
F:272,321,428/Active site: His, Asp, Ser #status predicted

Query Match 64.4%; Score 38; DB 1; Length 477;
Best Local Similarity 66.7%; Pred. No. 40;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 RLRSGEPC 10
:||| |||

Db 326 QLKSGSPQC 334

RESULT 8

JS0598
t-plasminogen activator (EC 3.4.21.68) alpha-2 precursor - common vampire bat
N:Alternate names: tissue plasminogen activator
C:Species: Desmodus rotundus (common vampire bat)
C>Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jul-1999
C:Accession: JS0598
R:Kraetzschmar, J.; Haendler, B.; Langer, G.; Boidol, W.; Bringmann, P.; Alagon, A.; Don
Gene 105, 229-237, 1991
A:Title: The plasminogen activator family from the salivary gland of the vampire bat Des
A:Reference number: JS0597; MUID:92039036; PMID:1937019
A:Accession: JS0598
A:Molecule type: mRNA
A:Residues: 1-477 <KRA>
A:Cross-references: GB:M63988; NID:gl66074; PIDN:AAA31593.1; PID:gl66075
C:Superfamily: tissue plasminogen activator; EGF homology; fibronectin type I repeat hom
C:Keywords: fibrinolysis; glycoprotein; hydrolase; kringle; serine proteinase
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-36/Domain: propeptide #status predicted <PRO>
F:37-477/Product: plasminogen activator alpha-2 #status predicted <PLA>
F:42-79/Domain: fibronectin type I repeat homology <IFR>
F:87-120/Domain: EGF homology <EGF>
F:128-209/Domain: kringle homology <KR>
F:226-471/Domain: trypsin homology <TRY>
F:42-72,70-79,87-98,92-109,111-120,128-209,149-191,180-204,214-345,257-273,265-334,359-4
F:185,398/Binding site: carbohydrate (Asn) (covalent) #status predicted

F:225-226/Cleavage site: His-Ser (plasmin) #status predicted
F:272,321,428/Active site: His, Asp, Ser #status predicted

Query Match 64.4%; Score 38; DB 2; Length 477;
Best Local Similarity 66.7%; Pred. No. 40;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 RLRSGEPC 10
:||| |||

Db 326 QLKSGSPQC 334

RESULT 9

A40044
PML-1 protein - human
N:Alternate names: promyelocytic leukemia protein
C:Species: Homo sapiens (man)
C>Date: 17-Aug-1992 #sequence_revision 17-Aug-1992 #text_change 02-Aug-2002
C:Accession: A40044
R:Kakizuka, A.; Miller Jr., W.H.; Umesono, K.; Warrell Jr., R.P.; Frankel, S.R.; Murt
Cell 66, 663-674, 1991
A:Title: Chromosomal translocation t(15;17) in human acute promyelocytic leukemia fus
A:Reference number: A40044; MUID:91347368; PMID:1652368
A:Accession: A40044
A:Molecule type: mRNA
A:Residues: 1-560 <KAK>
A:Cross-references: GB:M73778; NID:gl90114; PIDN:AAA60125.1; PID:gl90115
C:Genetics:
A:Gene: GDB:PML; MYL
A:Cross-references: GDB:127542; OMIM:102578
A:Map position: 15q22-15q22
C:Superfamily: human PML-1 protein; RING finger homology
C:Keywords: DNA binding; transcription regulation; zinc
F:53-97/Domain: RING finger homology <RNG>

Query Match 64.4%; Score 38; DB 2; Length 560;
Best Local Similarity 77.8%; Pred. No. 46;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CRLRSGEPQ 9
||||| |||

Db 357 CRLRQEPQ 365

RESULT 10

A60198
Myl protein - human
C:Species: Homo sapiens (man)
C>Date: 20-Feb-1993 #sequence_revision 20-Feb-1993 #text_change 02-Aug-2002
C:Accession: A60198
R:Pandolfi, P.P.; Grignani, F.; Alcalay, M.; Mencarelli, A.; Biondi, A.; Lococo, F.;
Oncogene 6, 1285-1292, 1991
A:Title: Structure and origin of the acute promyelocytic leukemia myl/RARalpha cDNA a
A:Reference number: A60198; MUID:91319412; PMID:1650447
A:Accession: A60198
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-589 <PAN>
A:Note: the authors' translation is shown for residues 543-549; the corresponding nuc
C:Superfamily: human PML-1 protein; RING finger homology
C:Keywords: zinc
F:31-75/Domain: RING finger homology <RNG>

Query Match 64.4%; Score 38; DB 2; Length 589;
Best Local Similarity 77.8%; Pred. No. 48;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CRLRSGEPQ 9
||||| |||

Db 335 CRLRQEPQ 343

RESULT 11

A::Title: The PML-RARalpha fusion mRNA generated by the t(15;17) translocation in acute promyelocytic leukemia

A::Reference number: A40045; MUID:91347369; PMID:1652369

A::Accession: B40045

A::Status: preliminary

A::Molecule type: mRNA

A::Residues: 1-593 <DE2>

C::Superfamily: human PML-1 protein; RING finger homology

C::Keywords: zinc

F:53-97/Domain: RING finger homology <RNG>

Query Match 64.4%; Score 38; DB 2; Length 593;

Best Local Similarity 77.8%; Pred. No. 49;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CRLRSGEPQ 9

Db 357 CRLRQEEPQ 365

||||| |||

RESULT 14

S19244

gene Myl protein - human

C::Species: Homo sapiens (man)

C::Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 02-Aug-2002

C::Accession: S19244

R::Kastner, P.; Perez, A.; Lutz, Y.; Rochette-Egly, C.; Gaub, M.P.; Durand, B.; Lanotti, E.M.B. J. 11, 629-642, 1992

A::Title: Structure, localization and transcriptional properties of two classes of retinoblastoma protein family of oncoproteins

A::Reference number: S19244; MUID:92164652; PMID:1311253

A::Accession: S19244

A::Status: preliminary

A::Molecule type: mRNA

A::Residues: 1-633 <KAS>

A::Cross-references: EMBL:X63131; NID:g34813; PIDN:CAA44841.1; PID:g34814

C::Superfamily: human PML-1 protein; RING finger homology

C::Keywords: DNA binding; transcription regulation; zinc

F:53-97/Domain: RING finger homology <RNG>

Query Match 64.4%; Score 38; DB 2; Length 633;

Best Local Similarity 77.8%; Pred. No. 52;

Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CRLRSGEPQ 9

Db 357 CRLRQEEPQ 365

||||| |||

RESULT 15

AG0252

probable DEAD box family helicase YPO2071 [imported] - Yersinia pestis (strain CO92)

C::Species: Yersinia pestis

C::Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 02-Nov-2001

C::Accession: AG0252

R::Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.; Deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Hill, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrett, N. Nature 413, 523-527, 2001

A::Title: Genome sequence of Yersinia pestis, the causative agent of plague.

A::Reference number: AB00001; MUID:21470413; PMID:11586360

A::Accession: AG0252

A::Status: preliminary

A::Molecule type: DNA

A::Residues: 1-634 <KUR>

A::Cross-references: GB:AL590842; PIDN:CAC90883.1; PID:g15980082; GSPDB:GN00175

C::Genetics:

A::Gene: YPO2071

Query Match 64.4%; Score 38; DB 2; Length 634;

Best Local Similarity 75.0%; Pred. No. 52;

Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CRLRSGEP 8

Db 557 CRLRGDP 564

||||| 1:1

Search completed: January 30, 2003, 13:33:21
Job time : 16 secs

13:40:38

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 30, 2003, 13:31:56 ; Search time 11 seconds
(without alignments)
37.706 Million cell updates/sec

Title: US-09-615-624A-1
Perfect score: 59
Sequence: 1 CRLRSGEPQC 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match % | Length | DB ID | Description |
|------------|-------|---------------|--------|--------------|---------------------|
| 1 | 45 | 76.3 | 3767 | MUA3_CAEEL | P34576 caenorhabdi |
| 2 | 41 | 69.5 | 798 | ITB1_HUMAN | P05556 homo sapien |
| 3 | 38.5 | 65.3 | 150 | RNK6_AOTR | O46528 aotus trivi |
| 4 | 38.5 | 65.3 | 150 | RNK6_CERAE | O46534 cercopithec |
| 5 | 38.5 | 65.3 | 150 | RNK6_GORGO | O46532 gorilla gor |
| 6 | 38.5 | 65.3 | 150 | RNK6_HUMAN | Q93091 homo sapien |
| 7 | 38.5 | 65.3 | 150 | RNK6_MACMU | O46533 macaca mula |
| 8 | 38.5 | 65.3 | 150 | RNK6_MIOTA | O46531 miopithecus |
| 9 | 38.5 | 65.3 | 150 | RNK6_PANTR | O46525 pan troglod |
| 10 | 38.5 | 65.3 | 150 | RNK6_PAPHA | O46527 papio hamad |
| 11 | 38.5 | 65.3 | 150 | RNK6_SAGOE | O46530 saguinus oe |
| 12 | 38 | 64.4 | 394 | URTG_DESRO | P49150 desmodus ro |
| 13 | 38 | 64.4 | 431 | URTB_DESRO | P98121 desmodus ro |
| 14 | 38 | 64.4 | 477 | URTB_DESRO | P15638 desmodus ro |
| 15 | 38 | 64.4 | 636 | YOAA_ECOLI | P76257 escherichia |
| 16 | 38 | 64.4 | 798 | ITB1_MOUSE | P09055 mus musculus |
| 17 | 38 | 64.4 | 799 | ITB1_RAT | P49134 rattus norv |
| 18 | 38 | 64.4 | 882 | ITB1_HUMAN | P53712 bos taurus |
| 19 | 37.5 | 63.6 | 150 | RNK6_SATSC | O46529 homo sapien |
| 20 | 37 | 62.7 | 64 | YSHB_CAEEL | O46529 saimiri sci |
| 21 | 37 | 62.7 | 393 | YSHB_CAEEL | O10027 caenorhabdi |
| 22 | 37 | 62.7 | 719 | DEND_RAT | O09949 caenorhabdi |
| 23 | 37 | 62.7 | 773 | ITB1_BOVIN | P50617 rattus norv |
| 24 | 37 | 62.7 | 798 | ITB1_FELCA | P53712 felis silve |
| 25 | 36.5 | 61.9 | 150 | RNK6_PONPY | O46526 pongo pygma |
| 26 | 36 | 61.0 | 472 | PHR_ECOLI | P00914 escherichia |
| 27 | 36 | 61.0 | 564 | NCAP_MACHU | P26578 machupo vir |
| 28 | 36 | 61.0 | 798 | ITB0_XENLA | P12607 xenopus lae |
| 29 | 36 | 61.0 | 798 | ITB1_XENLA | P12606 xenopus lae |
| 30 | 36 | 61.0 | 2768 | 1 THYG_HUMAN | P01266 homo sapien |
| 31 | 35 | 59.3 | 121 | RNL2_CHICK | P81476 gallus gall |
| 32 | 35 | 59.3 | 283 | 1 GSPK_XANCP | P34026 xanthomonas |
| 33 | 35 | 59.3 | 332 | 1 CLC3_CAVPO | Q9qzy6 cavia porce |

ALIGNMENTS

RESULT 1

| ID | MUA3_CAEEL | STANDARD; | PRT; | 3767 AA. |
|-----|---|-----------|------|----------|
| AC | P34576; Q9UAI3; Q21340; | | | |
| DT | 01-FEB-1994 (Rel. 28, Created) | | | |
| DT | 15-JUN-2002 (Rel. 41, Last sequence update) | | | |
| DT | 15-JUN-2002 (Rel. 41, Last annotation update) | | | |
| DE | Transmembrane cell adhesion receptor mua-3 precursor. | | | |
| GN | MUA-3 OR K08E5.3/720G5.3. | | | |
| OS | Caenorhabditis elegans. | | | |
| OC | Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae; Caenorhabditis. | | | |
| OC | Rhabditidae; Peloderinae; Caenorhabditis. | | | |
| OX | NCBI_TaxID=6239; | | | |
| RN | [1] | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RC | STRAIN=Bristol N2; | | | |
| RA | Lu Z., Vogel B., Hedgecock E.; | | | |
| RT | "mua-3 mRNA splicing pattern revealed." | | | |
| RL | Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases. | | | |
| [2] | | | | |
| RP | SEQUENCE FROM N.A. | | | |
| RC | STRAIN=Bristol N2; | | | |
| RA | Berks M., Smith A., Kershaw J.K.; | | | |
| RL | Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases. | | | |
| CC | - FUNCTION: Involved in cell adhesion. | | | |
| CC | - SIMILARITY: CONTAINS 52 EGF-LIKE DOMAINS. | | | |
| CC | - SIMILARITY: CONTAINS 2 LDL-RECEPTOR CLASS A DOMAINS. | | | |
| CC | - SIMILARITY: CONTAINS 2 SEA DOMAINS. | | | |
| CC | - SIMILARITY: CONTAINS 1 VWFA DOMAIN. | | | |
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| DR | EMBL; AF139060; AAD29428.1; | | | |
| DR | EMBL; Z30974; CAA83226.2; | | | |
| DR | EMBL; Z30423; CAA83226.2; JOINED. | | | |
| DR | EMBL; Z30423; CAC42345.1; | | | |
| DR | EMBL; Z30974; CAC42345.1; JOINED. | | | |
| DR | PIR; S42373; S42373. | | | |
| DR | HSSP; PI7301; IAOX. | | | |
| DR | WormPep; K08E5.3; CE28049. | | | |
| DR | InterPro; IPR000152; Asx_hydroxyl. | | | |
| DR | InterPro; IPR001762; Disintegrin. | | | |
| DR | InterPro; IPR000561; EGF-like. | | | |
| DR | InterPro; IPR001881; EGF-Ca. | | | |
| DR | InterPro; IPR002172; LDL_recept_A. | | | |
| DR | InterPro; IPR000082; SEA_domain. | | | |
| DR | InterPro; IPR002035; VWF_A. | | | |
| DR | Pfam; PF000008; EGF; 33. | | | |
| DR | Pfam; PF000057; ldl_recept_a; 3. | | | |
| DR | Pfam; PF01390; SEA; 2. | | | |

P28797 cavia porce
P08923 mus musculus
P46023 lymanaea sta
P55268 homo sapien
O61292 mus musculus
P15800 rattus norv
O61001 mus musculus
O84963 macaca mula
P24728 autographa
P44680 haemophilus
P49747 homo sapien
Q43847 solanum tub

| DR | Pfam; PR00092; vwa; 1. | FT | DOMAIN | 2763 | 2811 | EGF-LIKE 45. |
|----|--|----|----------|------|------|---|
| DR | PRINTS: PR00289; DISINTEGRIN. | FT | DOMAIN | 2833 | 2872 | EGF-LIKE 46. |
| DR | PRINTS: PR00261; LDLRECEPTOR. | FT | DOMAIN | 2873 | 2997 | SEA 1. |
| DR | PRINTS: PR00453; VWFA DOMAIN. | FT | DOMAIN | 3009 | 3048 | EGF-LIKE 47. |
| DR | SMART; SM00179; EGF_CA; 1. | FT | DOMAIN | 3049 | 3172 | SEA 2. |
| DR | SMART; SM00001; EGF_LIKE; 45. | FT | DOMAIN | 3176 | 3220 | EGF-LIKE 48. |
| DR | SMART; SM00192; LDL; 4. | FT | DOMAIN | 3224 | 3272 | EGF-LIKE 49. |
| DR | SMART; SM00200; SEA; 2. | FT | DOMAIN | 3272 | 3324 | EGF-LIKE 50. |
| DR | SMART; SM00327; VWA; 1. | FT | DOMAIN | 3328 | 3373 | EGF-LIKE 51, CALCIUM-BINDING (POTENTIAL). |
| DR | PROSITE; PS00010; ASX_HYDROXYL; 32. | FT | DOMAIN | 3373 | 3409 | EGF-LIKE 52. |
| DR | PROSITE; PS00022; EGF_1; 1. | FT | DISULFID | 229 | 243 | BY SIMILARITY. |
| DR | PROSITE; PS01186; EGF_2; 6. | FT | DISULFID | 235 | 252 | BY SIMILARITY. |
| DR | PROSITE; PS01187; EGF_CA; 1. | FT | DISULFID | 254 | 267 | BY SIMILARITY. |
| DR | PROSITE; PS50068; LDLRA_2; 4. | FT | DISULFID | 381 | 392 | BY SIMILARITY. |
| DR | PROSITE; PS50024; SEA; 2. | FT | DISULFID | 386 | 402 | BY SIMILARITY. |
| DR | PROSITE; PS50234; VWFA; 2. | FT | DISULFID | 404 | 415 | BY SIMILARITY. |
| KW | Receptor; Cell adhesion; EGF-like domain; Repeat; Transmembrane; | FT | DISULFID | 422 | 435 | BY SIMILARITY. |
| KW | Glycoprotein; Signal. | FT | DISULFID | 429 | 444 | BY SIMILARITY. |
| FT | SIGNAL | FT | DISULFID | 446 | 465 | BY SIMILARITY. |
| FT | CHAIN | FT | DISULFID | 472 | 486 | BY SIMILARITY. |
| FT | 25 | FT | DISULFID | 480 | 495 | BY SIMILARITY. |
| FT | 3176 | FT | DISULFID | 497 | 516 | BY SIMILARITY. |
| FT | 25 | FT | DISULFID | 523 | 536 | BY SIMILARITY. |
| FT | 3417 | FT | DISULFID | 530 | 545 | BY SIMILARITY. |
| FT | 3418 | FT | DISULFID | 547 | 565 | BY SIMILARITY. |
| FT | 3438 | FT | DISULFID | 571 | 588 | BY SIMILARITY. |
| FT | 3439 | FT | DISULFID | 588 | 605 | BY SIMILARITY. |
| FT | 3767 | FT | DISULFID | 618 | 632 | BY SIMILARITY. |
| FT | 63 | FT | DISULFID | 632 | 642 | BY SIMILARITY. |
| FT | 132 | FT | DISULFID | 642 | 662 | BY SIMILARITY. |
| FT | 166 | FT | DISULFID | 662 | 682 | BY SIMILARITY. |
| FT | 209 | FT | DISULFID | 682 | 691 | BY SIMILARITY. |
| FT | 268 | FT | DISULFID | 691 | 712 | BY SIMILARITY. |
| FT | 416 | FT | DISULFID | 712 | 729 | BY SIMILARITY. |
| FT | 466 | FT | DISULFID | 729 | 738 | BY SIMILARITY. |
| FT | 468 | FT | DISULFID | 738 | 759 | BY SIMILARITY. |
| FT | 519 | FT | DISULFID | 759 | 779 | BY SIMILARITY. |
| FT | 566 | FT | DISULFID | 779 | 788 | BY SIMILARITY. |
| FT | 614 | FT | DISULFID | 788 | 809 | BY SIMILARITY. |
| FT | 663 | FT | DISULFID | 809 | 836 | BY SIMILARITY. |
| FT | 713 | FT | DISULFID | 836 | 845 | BY SIMILARITY. |
| FT | 714 | FT | DISULFID | 845 | 859 | BY SIMILARITY. |
| FT | 760 | FT | DISULFID | 859 | 879 | BY SIMILARITY. |
| FT | 762 | FT | DISULFID | 879 | 888 | BY SIMILARITY. |
| FT | 810 | FT | DISULFID | 888 | 907 | BY SIMILARITY. |
| FT | 860 | FT | DISULFID | 907 | 930 | BY SIMILARITY. |
| FT | 861 | FT | DISULFID | 930 | 939 | BY SIMILARITY. |
| FT | 908 | FT | DISULFID | 939 | 960 | BY SIMILARITY. |
| FT | 910 | FT | DISULFID | 960 | 981 | BY SIMILARITY. |
| FT | 961 | FT | DISULFID | 981 | 990 | BY SIMILARITY. |
| FT | 1012 | FT | DISULFID | 990 | 1011 | BY SIMILARITY. |
| FT | 1029 | FT | DISULFID | 1011 | 1046 | BY SIMILARITY. |
| FT | 1071 | FT | DISULFID | 1046 | 1055 | BY SIMILARITY. |
| FT | 1120 | FT | DISULFID | 1055 | 1069 | BY SIMILARITY. |
| FT | 1168 | FT | DISULFID | 1069 | 1087 | BY SIMILARITY. |
| FT | 1219 | FT | DISULFID | 1087 | 1096 | BY SIMILARITY. |
| FT | 1219 | FT | DISULFID | 1096 | 1117 | BY SIMILARITY. |
| FT | 1406 | FT | DISULFID | 1117 | 1137 | BY SIMILARITY. |
| FT | 1406 | FT | DISULFID | 1137 | 1146 | BY SIMILARITY. |
| FT | 1421 | FT | DISULFID | 1146 | 1167 | BY SIMILARITY. |
| FT | 1466 | FT | DISULFID | 1167 | 1188 | BY SIMILARITY. |
| FT | 1466 | FT | DISULFID | 1188 | 1197 | BY SIMILARITY. |
| FT | 1510 | FT | DISULFID | 119 | | |

| DR | Pfam; PF00092; vwa; 1. | FT | DOMAIN | 2763 | 2811 | EGF-LIKE 45. |
|----|--|----|----------|------|------|---|
| DR | PRINTS: PR00289; DISINTEGRIN. | FT | DOMAIN | 2833 | 2872 | EGF-LIKE 46. |
| DR | PRINTS: PR00261; LDLRECEPTOR. | FT | DOMAIN | 2873 | 2997 | SEA 1. |
| DR | PRINTS: PR00453; VWFADOMAIN. | FT | DOMAIN | 3009 | 3048 | EGF-LIKE 47. |
| DR | SMART; SM00179; EGF_CA; 1. | FT | DOMAIN | 3049 | 3172 | SEA 2. |
| DR | SMART; SM00001; EGF_LIKE; 45. | FT | DOMAIN | 3176 | 3220 | EGF-LIKE 48. |
| DR | SMART; SM00192; LDL; 4. | FT | DOMAIN | 3224 | 3272 | EGF-LIKE 49. |
| DR | SMART; SM00200; SEA; 2. | FT | DOMAIN | 3272 | 3324 | EGF-LIKE 50. |
| DR | SMART; SM00327; VWA; 1. | FT | DOMAIN | 3328 | 3373 | EGF-LIKE 51, CALCIUM-BINDING (POTENTIAL). |
| DR | PROSITE; PS00010; ASX_HYDROXYL; 32. | FT | DOMAIN | 3373 | 3409 | EGF-LIKE 52. |
| DR | PROSITE; PS00022; EGF_1; 1. | FT | DISULFID | 229 | 243 | BY SIMILARITY. |
| DR | PROSITE; PS01186; EGF_2; 6. | FT | DISULFID | 235 | 252 | BY SIMILARITY. |
| DR | PROSITE; PS01187; EGF_CA; 1. | FT | DISULFID | 254 | 267 | BY SIMILARITY. |
| DR | PROSITE; PS50068; LDLRA_2; 4. | FT | DISULFID | 381 | 392 | BY SIMILARITY. |
| DR | PROSITE; PS50024; SEA; 2. | FT | DISULFID | 386 | 402 | BY SIMILARITY. |
| DR | PROSITE; PS50234; VWFA; 2. | FT | DISULFID | 404 | 415 | BY SIMILARITY. |
| KW | Receptor; Cell adhesion; EGF-like domain; Repeat; Transmembrane; | FT | DISULFID | 422 | 435 | BY SIMILARITY. |
| KW | Glycoprotein; Signal. | FT | DISULFID | 429 | 444 | BY SIMILARITY. |
| FT | SIGNAL | FT | DISULFID | 446 | 465 | BY SIMILARITY. |
| FT | CHAIN | FT | DISULFID | 472 | 486 | BY SIMILARITY. |
| FT | 25 | FT | DISULFID | 480 | 495 | BY SIMILARITY. |
| FT | 317 | FT | DISULFID | 497 | 516 | BY SIMILARITY. |
| FT | 3417 | FT | DISULFID | 523 | 536 | BY SIMILARITY. |
| FT | 3418 | FT | DISULFID | 530 | 545 | BY SIMILARITY. |
| FT | 3438 | FT | DISULFID | 547 | 565 | BY SIMILARITY. |
| FT | 3439 | FT | DISULFID | 565 | 582 | BY SIMILARITY. |
| FT | 3767 | FT | DISULFID | 618 | 632 | BY SIMILARITY. |
| FT | 63 | FT | DISULFID | 626 | 642 | BY SIMILARITY. |
| FT | 132 | FT | DISULFID | 644 | 662 | BY SIMILARITY. |
| FT | 166 | FT | DISULFID | 669 | 682 | BY SIMILARITY. |
| FT | 209 | FT | DISULFID | 676 | 691 | BY SIMILARITY. |
| FT | 258 | FT | DISULFID | 693 | 712 | BY SIMILARITY. |
| FT | 416 | FT | DISULFID | 718 | 729 | BY SIMILARITY. |
| FT | 466 | FT | DISULFID | 723 | 738 | BY SIMILARITY. |
| FT | 468 | FT | DISULFID | 740 | 759 | BY SIMILARITY. |
| FT | 517 | FT | DISULFID | 756 | 779 | BY SIMILARITY. |
| FT | 566 | FT | DISULFID | 773 | 788 | BY SIMILARITY. |
| FT | 614 | FT | DISULFID | 790 | 809 | BY SIMILARITY. |
| FT | 663 | FT | DISULFID | 820 | 836 | BY SIMILARITY. |
| FT | 713 | FT | DISULFID | 828 | 845 | BY SIMILARITY. |
| FT | 714 | FT | DISULFID | 847 | 859 | BY SIMILARITY. |
| FT | 760 | FT | DISULFID | 855 | 879 | BY SIMILARITY. |
| FT | 762 | FT | DISULFID | 873 | 888 | BY SIMILARITY. |
| FT | 816 | FT | DISULFID | 890 | 907 | BY SIMILARITY. |
| FT | 860 | FT | DISULFID | 914 | 930 | BY SIMILARITY. |
| FT | 861 | FT | DISULFID | 924 | 939 | BY SIMILARITY. |
| FT | 908 | FT | DISULFID | 941 | 960 | BY SIMILARITY. |
| FT | 910 | FT | DISULFID | 967 | 981 | BY SIMILARITY. |
| FT | 961 | FT | DISULFID | 975 | 990 | BY SIMILARITY. |
| FT | 1012 | FT | DISULFID | 992 | 1011 | BY SIMILARITY. |
| FT | 1029 | FT | DISULFID | 1033 | 1046 | BY SIMILARITY. |
| FT | 1071 | FT | DISULFID | 1040 | 1055 | BY SIMILARITY. |
| FT | 1120 | FT | DISULFID | 1057 | 1069 | BY SIMILARITY. |
| FT | 1168 | FT | DISULFID | 1075 | 1087 | BY SIMILARITY. |
| FT | 1219 | FT | DISULFID | 1081 | 1096 | BY SIMILARITY. |
| FT | 1219 | FT | DISULFID | 1098 | 1117 | BY SIMILARITY. |
| FT | 1406 | FT | DISULFID | 1124 | 1137 | BY SIMILARITY. |
| FT | 1421 | FT | DISULFID | 1131 | 1146 | BY SIMILARITY. |
| FT | 1466 | FT | DISULFID | 1148 | 1167 | BY SIMILARITY. |
| FT | 1466 | FT | DISULFID | 1174 | 1188 | BY SIMILARITY. |
| FT | 1510 | FT | DISULFID | 1182 | 1197 | BY SIMILARITY. |
| FT | 1521 | FT | DISULFID | 1199 | 1218 | BY SIMILARITY. |
| FT | 1562 | FT | DISULFID | | | |

Query Match 76.3%; Score 45; DB 1; Length 3767;
 Best Local Similarity 70.0%; Pred. No. 4.2;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CRLRSGPQC 10
 ||| |||:
 Db 2088 CRLMGEPKC 2057

RESULT 2

ITB1_HUMAN STANDARD; PRT: 798 AA.
 AC P05556; P78466; Q13089; Q14647; Q13090; Q13212; Q13091;
 AC Q14622;
 DT 01-NOV-1988 (Rel. 09, Created)
 DT 01-NOV-1988 (Rel. 09, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Integrin beta-1 precursor (Fibronectin receptor beta subunit)
 DE (CD29 antigen) (Integrin VLA-4 beta subunit);
 GN ITGB1 OR FNBR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORM BETA-1A).
 RC TISSUE=Placenta;
 RX MEDLINE=88007843; PubMed=2958481;
 RA Agraves W.S., Suzuki S., Arai H., Thompson K., Pierschbacher M.D.,
 RA Ruoslahti E.;
 RT "Amino acid sequence of the human fibronectin receptor.";
 RL J. Cell Biol. 105:1183-1190(1987).
 RN [2]
 RP SEQUENCE OF 717-757 FROM N.A., AND CHARACTERIZATION OF BETA-1B.
 RX MEDLINE=93209984; PubMed=7681433;
 RA Balzac F., Belkin A.M., Koteliarsky V.E., Balabanov Y.V., Altruda F.,
 RA Silengo L., Tarone G.;
 RT "Expression and functional analysis of a cytoplasmic domain variant of
 the beta 1 integrin subunit.";
 RL J. Cell Biol. 121:171-178(1993).
 RN [3]
 RP SEQUENCE OF 717-757 FROM N.A., AND FUNCTION.
 RX MEDLINE=95014744; PubMed=7523423;
 RA Balzac F., Retta S.F., Albini A., Melchiorri A., Koteliarsky V.E.,
 RA Geuna M., Silengo L., Tarone G.;
 RT "Expression of beta 1B integrin isoform in CHO cells results in a
 dominant negative effect on cell adhesion and motility.";
 RL J. Cell Biol. 127:557-565(1994).
 RN [4]
 RP PARTIAL SEQUENCE FROM N.A. (ISOFORMS BETA-1A; BETA-1B; BETA-1C AND
 RP BETA-1D).
 RC TISSUE=Skeletal muscle;
 RX MEDLINE=95398646; PubMed=7545396;
 RA Zhidkova N.I., Belkin A.M., Mayne R.;
 RT "Novel isoform of beta 1 integrin expressed in skeletal and cardiac
 muscle.";
 RL Biochem. Biophys. Res. Commun. 214:279-285(1995).
 RN [5]
 RP PARTIAL SEQUENCE FROM N.A. (ISOFORM BETA-1B).
 RC TISSUE=Skeletal muscle;
 RX MEDLINE=91065539; PubMed=2249781;
 RA Altruda F., Cervella P., Tarone G., Botta C., Balzac F., Stefanuto G.,
 RA Silengo L.;
 RT "A human integrin beta 1 subunit with a unique cytoplasmic domain
 generated by alternative mRNA processing.";
 RL Gene 95:261-266(1990).
 RN [6]
 RP PARTIAL SEQUENCE FROM N.A. (ISOFORM BETA-1D).
 RX MEDLINE=95377431; PubMed=7544298;
 RA van der Flier A., Kuikman I., Baudoin C., van der Neut R.,
 RA Sonnenberg A.;
 RT "A novel beta 1 integrin isoform produced by alternative splicing:

RT unique expression in cardiac and skeletal muscle.";
 RL REBS Lett. 369:340-344(1995).
 RN [7]
 RP PARTIAL SEQUENCE FROM N.A. (ISOFORMS BETA-1A AND BETA-1C).
 RC TISSUE=Cervical carcinoma;
 RX MEDLINE=92202779; PubMed=1551917;
 RA Languino L.R., Ruoslahti E.;
 RT "An alternative form of the integrin beta 1 subunit with a variant
 cytoplasmic domain.";
 RL J. Biol. Chem. 267:7116-7120(1992).
 RN [8]
 RP PARTIAL SEQUENCE FROM N.A. (ISOFORM BETA-1C-2).
 RX MEDLINE=98161805; PubMed=9494094;
 RA Svineng G., Faessler R., Johansson S.;
 RT "Identification of beta1c-2, a novel variant of the integrin beta1
 subunit generated by utilization of an alternative splice acceptor
 site in exon C.";
 RL Biochem. J. 330:1255-1263(1998).
 CC -1- FUNCTION: INTEGRINS ALPHA-1/BETA-1, ALPHA-2/BETA-1, ALPHA-10/BETA-1
 CC 1 AND ALPHA-11/BETA-1 ARE RECEPTORS FOR COLLAGEN. INTEGRINS ALPHA-
 CC 1/BETA-1 AND ALPHA-2/BETA-2 RECOGNIZE THE PROLINE-HYDROXYLATED
 CC SEQUENCE G-F-P-G-E-R IN COLLAGEN. INTEGRINS ALPHA-2/BETA-1, ALPHA-
 CC 3/BETA-1, ALPHA-4/BETA-1, ALPHA-5/BETA-1, ALPHA-8/BETA-1, ALPHA-
 CC 10/BETA-1, ALPHA-11/BETA-1 AND ALPHA-V/BETA-1 ARE RECEPTORS FOR
 CC FIBRONECTIN. ALPHA-4/BETA-1 RECOGNIZES ONE OR MORE DOMAINS WITHIN
 CC THE ALTERNATIVELY SPLICED CS-1 AND CS-5 REGIONS OF FIBRONECTIN.
 CC INTEGRIN ALPHA-5/BETA-1 IS A RECEPTOR FOR FIBRINOGEN. INTEGRIN
 CC ALPHA-1/BETA-1, ALPHA-2/BETA-1, ALPHA-6/BETA-1 AND ALPHA-7/BETA-1
 CC ARE RECEPTORS FOR LAMININ. INTEGRIN ALPHA-4/BETA-1 IS A RECEPTOR
 CC FOR VCAM1. IT RECOGNIZES THE SEQUENCE Q-I-D-S IN VCAM1. INTEGRIN
 CC ALPHA-9/BETA-1 IS A RECEPTOR FOR VCAM1, CYTOTACTIN AND
 CC OSTOPONTIN. IT RECOGNIZES THE SEQUENCE A-E-I-D-G-I-E-L IN
 CC CYTOTACTIN. INTEGRIN ALPHA-3/BETA-1 IS A RECEPTOR FOR EPLINORIN
 CC AND THROMBOSPONDIN. INTEGRIN ALPHA-V/BETA-1 IS A RECEPTOR FOR
 CC VITRONECTIN. BETA-1 INTEGRINS RECOGNIZE THE SEQUENCE R-G-D IN A
 CC WIDE ARRAY OF LIGANDS. ISOFORM BETA-1B INTERFERES WITH ISOFORM
 CC BETA-1A RESULTING IN A DOMINANT NEGATIVE EFFECT ON CELL ADHESION
 CC AND MIGRATION (IN VITRO).
 CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT. BETA-1
 CC ASSOCIATES WITH EITHER ALPHA-1, ALPHA-2, ALPHA-3, ALPHA-4, ALPHA-
 CC 5, ALPHA-6, ALPHA-7, ALPHA-8, ALPHA-9, ALPHA-10, ALPHA-11 OR
 CC ALPHA-V.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. ISOFORM BETA-1B
 CC DOES NOT LOCALIZE TO FOCAL ADHESIONS.
 CC -1- ALTERNATIVE PRODUCTS: 5 ISOFORMS; BETA-1A (SHOWN HERE), BETA-1B,
 CC BETA-1C, BETA-1C-2 AND BETA-1D; ARE PRODUCED BY ALTERNATIVE
 CC SPLICING.
 CC -1- TISSUE SPECIFICITY: ISOFORM BETA-1A IS WIDELY EXPRESSED, OTHER
 CC ISOFORMS ARE GENERALLY COEXPRESSED WITH A MORE RESTRICTED
 CC DISTRIBUTION. ISOFORM BETA-1B IS EXPRESSED IN SKIN, LIVER,
 CC SKELETAL MUSCLE, CARDIAC MUSCLE, PLACENTA, UMBILICAL VEIN
 CC ENDOTHELIAL CELLS, NEUROBLASTOMA CELLS, LYMPHOMA CELLS, HEPATOMA
 CC CELLS AND ASTROCYTOMA CELLS. ISOFORMS BETA-1C AND BETA-1C-2 ARE
 CC EXPRESSED IN MUSCLE, KIDNEY, LIVER, PLACENTA, CERVICAL EPITHELIUM,
 CC UMBILICAL VEIN ENDOTHELIAL CELLS, FIBROBLAST CELLS, EMBRYONAL
 CC KIDNEY CELLS, PLATELETS AND SEVERAL BLOOD CELL LINES. ISOFORM
 CC BETA-1C-2, RATHER THAN ISOFORM BETA-1C, IS SELECTIVELY EXPRESSED IN
 CC PRIMARY T-CELLS. ISOFORM BETA-1C IS EXPRESSED IN NONPROLIFERATING
 CC AND DIFFERENTIATED PROSTATE GLAND EPITHELIAL CELLS. ISOFORM BETA-
 CC 1D IS EXPRESSED SPECIFICALLY IN STRIATED MUSCLE (SKELETAL AND
 CC CARDIAC MUSCLE).
 CC -1- SIMILARITY: BELONGS TO THE INTEGRIN BETA CHAIN FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 VNFA-LIKE DOMAIN.
 CC -1- DATABASE: NAME=PROV; NOTE=CD guide CD29 entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd29.htm".
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CC EMBL: X07979; CAA30790.1; -
DR EMBL: U33882; AAA79835.1; -
DR EMBL: U33875; AAA79835.1; JOINED.
DR EMBL: M84237; AAA74402.1; -
DR EMBL: U33879; AAA79832.1; -
DR EMBL: M34189; AAA59182.1; -
DR EMBL: U33880; AAA79833.1; -
DR EMBL: U33879; AAA79833.1; JOINED.
DR EMBL: U28252; AAA81366.1; -
DR EMBL: U33882; AAA79834.1; -
DR EMBL: U33879; AAA79834.1; JOINED.
DR EMBL: U33881; AAA79834.1; JOINED.
DR EMBL: M84237; AAA74403.1; -
DR EMBL: B27079; B27079.
DR Genew: HGNC.6153; ITGB1.
DR MIM: 135630; -
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR002369; Integrin_B.
DR InterPro: IPR001169; Integrin_beta_C.
DR InterPro: IPR003659; Plexin-like.
DR InterPro: IPR002035; VWF_A.
DR Pfam: PF00362; Integrin_B.
DR PRINTS: P01186; INTEGRINB.
DR PRODOM: PD001811; Integrin_B; 1.
DR SMART: SM00001; EGF_like; 1.
DR SMART: SM00187; INB; 1.
DR SMART: SM00423; PSI; 1.
DR SMART: SM00423; VWA; 1.
DR SMART: SM00327; VWA; 1.
DR PROSITE: PS00243; INTEGRIN_BETA; 3.
DR PROSITE: PS00042; EGF_1; UNKNOWN.2.
DR InterPro: IPR000561; Integrin_beta_C.
KW Repeat; Cell adhesion; Receptor; Transmembrane; Glycoprotein;
KW Repeat; Signal; Phosphorylation; Alternative splicing.
FT SIGNAL 1 20
FT CHAIN 21 798
FT DOMAIN 21 798 INTEGRIN BETA-1.
FT TRANSFEM 729 751 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 729 751 POTENTIAL.
FT DOMAIN 752 798 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 140 378 VWA-LIKE.
FT DOMAIN 466 635 4 CYSTEINE-RICH TANDEM REPEATS.
FT REPEAT 466 515 I.
FT REPEAT 516 559 II.
FT REPEAT 560 598 III.
FT REPEAT 599 635 IV.
FT DISULFID 27 464 BY SIMILARITY.
FT DISULFID 35 45 BY SIMILARITY.
FT DISULFID 38 75 BY SIMILARITY.
FT DISULFID 207 213 BY SIMILARITY.
FT DISULFID 261 301 BY SIMILARITY.
FT DISULFID 401 415 BY SIMILARITY.
FT DISULFID 435 691 BY SIMILARITY.
FT DISULFID 462 466 BY SIMILARITY.
FT DISULFID 477 489 BY SIMILARITY.
FT DISULFID 486 525 BY SIMILARITY.
FT DISULFID 491 500 BY SIMILARITY.
FT DISULFID 502 516 BY SIMILARITY.
FT DISULFID 531 536 BY SIMILARITY.
FT DISULFID 533 568 BY SIMILARITY.
FT DISULFID 538 553 BY SIMILARITY.
FT DISULFID 555 560 BY SIMILARITY.
FT DISULFID 574 579 BY SIMILARITY.
FT DISULFID 576 607 BY SIMILARITY.
FT DISULFID 581 590 BY SIMILARITY.
FT DISULFID 592 599 BY SIMILARITY.
FT DISULFID 613 618 BY SIMILARITY.

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Query Match 69.5%; Score 41; DB 1; Length 798;
Best Local Similarity 100.0%; Pred. No. 4.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RLRSGEPO 9
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Db 122 RLRSGEPO 129

RESULT 3
RNK6_AOTTR STANDARD; PRT; 150 AA.
AC O46528;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Ribonuclease K6 precursor (EC 3.1.27.-) (RNase K6).
GN RNASE6.
OS Aotus trivirgatus (Night monkey) (Douroucouli).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Aotus.
OC NCBI_TaxID=9505;
OX [1]
RN SEQUENCE FROM N.A.
RP MEDLINE=98311672; PubMed=9647635;
RA Deming M.S., Dyer K.D., Bankier A.T., Piper M.B., Dear P.H.,
RA Rosenberg H.F.;
RT "Ribonuclease k6: chromosomal mapping and divergent rates of
RT evolution within the RNase A gene superfamily.";
RL Genome Res. 8:599-607(1998).
CC -!- FUNCTION: MAY HAVE A ROLE IN HOST DEFENSE.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AF037084; AAB94746.1; -
CC HSP: P00656; ISSA.
DR InterPro: IPR001427; RNaseA.
DR Pfam: PF00074; RNaseA; 1.
DR PRINTS: P00794; RIBONUCLEASE.
DR PRODOM: PD000535; RNaseA; 1.
DR SMART: SM00092; RNase_Pc; 1.
DR PROSITE: PS00127; RNASE_PANCREATIC; 1.
KW Hydrolase; Nuclease; Endonuclease; Signal; Glycoprotein.
FT SIGNAL 1 23 BY SIMILARITY.
FT CHAIN 24 150 RIBONUCLEASE K6.
FT ACT_SITE 38 61 BY SIMILARITY.
FT ACT_SITE 61 61 BY SIMILARITY.
FT ACT_SITE 145 145 BY SIMILARITY.
FT DISULFID 46 104 BY SIMILARITY.
FT DISULFID 60 114 BY SIMILARITY.
FT DISULFID 78 129 BY SIMILARITY.
FT DISULFID 85 92 BY SIMILARITY.
FT CARBOHYD 55 55 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 100 100 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 150 AA; 17034 MW; C20D36C673C1A495 CRC64;
Query Match 65.3%; Score 38.5; DB 1; Length 150;
Best Local Similarity 72.7%; Pred. No. 2.5;
Matches 8; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 CRLRSGE-POC 10
|||||
Db 104 CRLTSGKYPQC 114

RESULT 4
RNK6_CERAE STANDARD; PRT; 150 AA.
AC O46534;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)

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RA Rosenberg H.F.;
RL Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: MAY HAVE A ROLE IN HOST DEFENSE.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: STRONG EXPRESSION IN LUNG, FOLLOWED BY HEART,
CC PLACENTA, KIDNEY, PANCREAS, LIVER, BRAIN AND SKELETAL MUSCLE. ALSO
CC EXPRESSED IN MONOCYTES AND NEUTROPHILS.
CC -!- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U64998; AAC51848.1;
CC HSSP: P00656; ILSQ.
CC Genew: HGNC:10048; RNASE6.
CC MIM: 601981;
CC InterPro: IPR001427; RNaseA.
CC Pfam: PF00074; rnasea.1.
CC PRINTS: PR00794; RIBONUCLEASE.
CC ProDom: PD000535; RNaseA; 1.
CC SMART: SM00092; RNaseA; 1.
CC PROSITE: PS00127; RNASE_PANCREATIC; 1.
CC Hydrolase; Nuclease; Endonuclease; Signal; Glycoprotein; Polymorphism.
CC KW SIGNAL 1 23 BY SIMILARITY.
CC FT CHAIN 24 150 RIBONUCLEASE K6.
CC FT ACT_SITE 38 38 BY SIMILARITY.
CC FT ACT_SITE 61 61 BY SIMILARITY.
CC FT ACT_SITE 145 145 BY SIMILARITY.
CC FT DISULFID 46 104 BY SIMILARITY.
CC FT DISULFID 60 114 BY SIMILARITY.
CC FT DISULFID 78 129 BY SIMILARITY.
CC FT DISULFID 85 92 BY SIMILARITY.
CC FT CARBOHYD 55 55 N-LINKED (GLCNAC...) (POTENTIAL).
CC FT CARBOHYD 100 100 N-LINKED (GLCNAC...) (POTENTIAL).
CC FT VARIANT 89 89 R -> Q (IN DBSNP:1045922).
CC FT /FTID=VAR_012048.
CC SQ SEQUENCE 150 AA; 17196 MW; 4C1F7220668CC13A CRC64;

Query Match 65.3%; Score 38.5; DB 1; Length 150;
Best Local Similarity 72.7%; Pred. No. 2.5;
Matches 8; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 CRLRSCE-PQC 10
DB 104 CRLTSGKYPQC 114

RESULT 7
RNK6_MACMU STANDARD; PRT; 150 AA.
AC O46533;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Ribonuclease K6 precursor (EC 3.1.27.-) (RNase K6).
GN RNASE6.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=98311672; PubMed=9647635;
RA Deming M.S., Dyer K.D., Bankier A.T., Piper M.B., Dear P.H.,
RA Rosenberg H.F.;
RT "Ribonuclease K6: chromosomal mapping and divergent rates of

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RT evolution within the RNase A gene superfamily.";
RL Genome Res. 8:599-607(1998).
CC -!- FUNCTION: MAY HAVE A ROLE IN HOST DEFENSE.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AF037089; AAB94751.1;
CC HSSP: P00656; ILSQ.
CC InterPro: IPR001427; RNaseA.
CC Pfam: PF00074; rnasea.1.
CC PRINTS: PR00794; RIBONUCLEASE.
CC ProDom: PD000535; RNaseA; 1.
CC SMART: SM00092; RNaseA; 1.
CC PROSITE: PS00127; RNASE_PANCREATIC; 1.
CC Hydrolase; Nuclease; Endonuclease; Signal; Glycoprotein.
CC KW SIGNAL 1 23 BY SIMILARITY.
CC FT CHAIN 24 150 RIBONUCLEASE K6.
CC FT ACT_SITE 38 38 BY SIMILARITY.
CC FT ACT_SITE 61 61 BY SIMILARITY.
CC FT ACT_SITE 145 145 BY SIMILARITY.
CC FT DISULFID 46 104 BY SIMILARITY.
CC FT DISULFID 60 114 BY SIMILARITY.
CC FT DISULFID 78 129 BY SIMILARITY.
CC FT DISULFID 85 92 BY SIMILARITY.
CC FT CARBOHYD 55 55 N-LINKED (GLCNAC...) (POTENTIAL).
CC FT CARBOHYD 100 100 N-LINKED (GLCNAC...) (POTENTIAL).
CC SQ SEQUENCE 150 AA; 17177 MW; 3144428106F759BB CRC64;

Query Match 65.3%; Score 38.5; DB 1; Length 150;
Best Local Similarity 72.7%; Pred. No. 2.5;
Matches 8; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 CRLRSCE-PQC 10
DB 104 CRLTSGKYPQC 114

RESULT 8
RNK6_MIOTA STANDARD; PRT; 150 AA.
AC O46531;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Ribonuclease K6 precursor (EC 3.1.27.-) (RNase K6).
GN RNASE6.
OS Miopithecus talapoin (Talapoin) (Cercopithecus talapoin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Miopithecus.
OX NCBI_TaxID=36231;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=98311672; PubMed=9647635;
RA Deming M.S., Dyer K.D., Bankier A.T., Piper M.B., Dear P.H.,
RA Rosenberg H.F.;
RT "Ribonuclease K6: chromosomal mapping and divergent rates of
RT evolution within the RNase A gene superfamily.";
RL Genome Res. 8:599-607(1998).
CC -!- FUNCTION: MAY HAVE A ROLE IN HOST DEFENSE.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
CC -----
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FT ACT_SITE 61 BY SIMILARITY.
FT ACT_SITE 145 BY SIMILARITY.
FT DISULFID 46 BY SIMILARITY.
FT DISULFID 60 BY SIMILARITY.
FT DISULFID 78 BY SIMILARITY.
FT DISULFID 85 BY SIMILARITY.
FT CARBOHYD 55 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 100 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 150 AA; 17237 MW; 463299F106F759AA CRC64;

Query Match 65.3%; Score 38.5; DB 1; Length 150;
Best Local Similarity 72.7%; Pred. No. 2.5;
Matches 8; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 CRLRSGE-POC 10
DB 104 CRLTSGKYPC 114

RESULT 11
RNK6_SAGOE
ID RNK6_SAGOE STANDARD; PRT; 150 AA.
AC O46530;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Ribonuclease K6 precursor (EC 3.1.27.-) (RNase K6).
GN RNASE6.
OS Saginus oedipus (Cotton-top tamarin).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Platyrrhini; Callitrichidae; Saginus.
OX NCBI_TaxID=9490;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98311672; PubMed=9647635;
RA Deming M.S., Dyer K.D., Bankier A.T., Piper M.B., Dear P.H.,
RA Rosenberg H.F.;
RT "Ribonuclease K6: chromosomal mapping and divergent rates of
RT evolution within the RNase A gene superfamily."
RL Genome Res. 8:599-607(1998).
CC -!- FUNCTION: MAY HAVE A ROLE IN HOST DEFENSE.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE PANCREATIC RIBONUCLEASE FAMILY.
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; AF037086; AAB94748.1; -
CC HSSP; P00656; 1SSA.
CC InterPro; IPR001427; RNaseA.
CC Pfam; PF00074; rnaase; 1.
CC PRINTS; PR00794; RIBONUCLEASE.
CC ProDom; PD000535; RNaseA; 1.
CC SMART; SM00092; RNasePc; 1.
CC PROSITE; PS00127; RNASE_PANCREATIC; 1.
KW Hydrolase; Nuclease; Endonuclease; Signal; Glycoprotein.
FT SIGNAL 1 23 BY SIMILARITY.
FT CHAIN 24 150 RIBONUCLEASE K6.
FT ACT_SITE 38 38 BY SIMILARITY.
FT ACT_SITE 61 61 BY SIMILARITY.
FT ACT_SITE 145 145 BY SIMILARITY.
FT DISULFID 46 104 BY SIMILARITY.
FT DISULFID 60 114 BY SIMILARITY.
FT DISULFID 78 129 BY SIMILARITY.
FT DISULFID 85 92 BY SIMILARITY.
FT CARBOHYD 55 55 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 150 AA; 17044 MW; 8B6AACAA8FAFE93 CRC64;

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Query Match 65.3%; Score 38.5; DB 1; Length 150;
Best Local Similarity 72.7%; Pred. No. 2.5;
Matches 8; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 CRLRSGE-POC 10
DB 104 CRLTSGKYPC 114

RESULT 12
URTG_DESRO
ID URTG_DESRO STANDARD; PRT; 394 AA.
AC P49150;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Salivary plasminogen activator gamma precursor (EC 3.4.21.68) (DSPA
DE gamma).
OS Desmodus rotundus (Vampire bat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Chiroptera; Microchiroptera; Phyllostomidae;
OC Desmodontinae; Desmodus.
OX NCBI_TaxID=9430;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Salivary gland;
RX MEDLINE=92039036; PubMed=1937019;
RA Kraetzschmar J., Haendler B., Langer G., Boidol W., Bringmann P.,
RA Alagon A., Donner P., Schleuning W.D.;
RT "The plasminogen activator family from the salivary gland of the
RT vampire bat Desmodus rotundus: cloning and expression."
RL Gene 105:229-237(1991).
RN [2]
RP CHARACTERIZATION.
RX MEDLINE=93393059; PubMed=1309059;
RA Schleuning W.-D., Alagon A., Boidol W., Bringmann P., Petri T.,
RA Kraetzschmar J., Haendler B., Langer G., Baldus B., Witt W.,
RA Donner P.;
RT "Plasminogen activators from the saliva of Desmodus rotundus (common
RT vampire bat): unique fibrin specificity."
RL Ann. N.Y. Acad. Sci. 667:395-403(1992).
CC -!- FUNCTION: PROBABLY ESSENTIAL TO SUPPORT THE FEEDING HABITS OF THIS
CC EXCLUSIVELY HAEMATOPHAGOUS ANIMAL. PROBABLE POTENT THROMBOLYTIC
CC AGENT.
CC -!- CATALYTIC ACTIVITY: Specific cleavage of Arg-I-Val bond in
CC plasminogen to form plasmin.
CC -!- SUBUNIT: MONOMER.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC -!- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M63990; AAA31595.1; -
CC HSSP; P98119; IAS1.
CC MEROPS; S01.239; -.
CC InterPro; IPR001314; Chymotrypsin.
CC InterPro; IPR000001; Kringle.
CC InterPro; IPR001254; Ser_protease_Try.
CC Pfam; PF00051; kringle; 1.
CC Pfam; PF00089; trypsin; 1.
CC PRINTS; PR00722; CHYMOTRYPSIN.
CC PRINTS; PR00018; KRINGLE.
CC ProDom; PD000395; Kringle; 1.
CC SMART; SM00130; KR; 1.
CC SMART; SM00020; Tryp-Spc; 1.
CC PROSITE; PS00021; KRINGLE_1; 1.

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DR PROSITE: PS50070; KRINGLE_2; 1.
 DR PROSITE: PS50240; TRYPSIN_DOM; 1.
 DR PROSITE: PS00134; TRYPSIN_HIS; 1.
 DR PROSITE: PS00135; TRYPSIN_SER; 1.
 KW Plasminogen activation; Hydrolase; Serine protease; Glycoprotein;
 KRingle; Signal; Multigene family.
 FT SIGNAL 1 36
 FT CHAIN 37 394
 FT DOMAIN 45 126
 FT ACT_SITE 142 394
 FT ACT_SITE 189 189
 FT ACT_SITE 238 238
 FT ACT_SITE 345 345
 FT ACT_SITE 345 345
 FT DISULFID 45 126
 FT DISULFID 66 108
 FT DISULFID 97 121
 FT DISULFID 131 262
 FT DISULFID 174 190
 FT DISULFID 182 251
 FT DISULFID 276 351
 FT DISULFID 308 324
 FT DISULFID 341 369
 FT CARBOHYD 315 315
 SQ SEQUENCE 394 AA; 44105 MW; 9CCD6F5F3D81FCD CRC64;
 Query Match 64.4%; Score 38; DB 1; Length 394;
 Best Local Similarity 66.7%; Pred. No. 8.4;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 2 RLRSGEPOC 10
 DB 243 QLKSGSPQC 251
 RESULT 13
 ID URTB_DESRO STANDARD; PRT; 431 AA.
 AC P98121;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Salivary plasminogen activator beta precursor (EC 3.4.21.68) (DSFA
 beta)
 OS Desmodus rotundus (Vampire bat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Chiroptera; Microchiroptera; Phyllostomidae;
 OC Desmodontinae; Desmodus.
 OX NCBI_TaxID=9430;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Salivary gland;
 RX MEDLINE=92039036; PubMed=1937019;
 RA Kraetzschmar J., Haendler B., Langer G., Boidol W., Bringmann P.,
 Alaon A., Donner P., Schleuning W.D.;
 FT "The plasminogen activator family from the salivary gland of the
 RT vampire bat Desmodus rotundus: cloning and expression.";
 RL Gene 105:229-237(1991).
 RN [2]
 RP CHARACTERIZATION.
 RX MEDLINE=93393059; PubMed=1309059;
 RA Schleuning W.-D., Alaon A., Boidol W., Bringmann P., Petri T.,
 RA Kraetzschmar J., Haendler B., Langer G., Baidus B., Witt W.,
 RA Donner P.;
 RT "Plasminogen activators from the saliva of Desmodus rotundus (common
 RT vampire bat): unique fibrin specificity.";
 RL Ann. N.Y. Acad. Sci. 667:395-403(1992).
 CC -!- FUNCTION: PROBABLY ESSENTIAL TO SUPPORT THE FEEDING HABITS OF THIS
 CC EXCLUSIVELY HAEMATOPHAGOUS ANIMAL. PROBABLE POTENT THROMBOLYTIC
 CC AGENT.
 CC -!- CATALYTIC ACTIVITY: Specific cleavage of Arg-1-Val bond in
 CC plasminogen to form plasmin.
 CC -!- SUBUNIT: MONOMER.
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.

CC -!- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
 CC -!- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
 CC -----
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 CC -----
 DR EMBL: M63989; AAA31594.1; -
 DR HSPSP; P98119; IASI.
 DR MEROPS; S01.239; -
 DR InterPro; IPR001314; Chymotrypsin.
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR000001; Kringle.
 DR InterPro; IPR001254; Ser_protease_Try.
 DR Pfam; PF00008; EGF; 1.
 DR Pfam; PF00051; kringle; 1.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00018; KRINGLE.
 DR ProDom; PD000395; Kringle; 1.
 DR SMART; SM00181; EGF; 1.
 DR SMART; SM00130; KR; 1.
 DR SMART; SM00020; Tryp_SPC; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; 1.
 DR PROSITE; PS00021; KRINGLE_1; 1.
 DR PROSITE; PS00070; KRINGLE_2; 1.
 DR PROSITE; PS50240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Plasminogen activation; Hydrolase; Serine protease; Glycoprotein;
 KW Kringle; EGF-like domain; Signal; Multigene family.
 FT SIGNAL 1 36
 FT CHAIN 37 431
 FT DOMAIN 37 75
 FT DOMAIN 82 163
 FT DOMAIN 179 431
 FT ACT_SITE 226 226
 FT ACT_SITE 275 275
 FT ACT_SITE 382 382
 FT DISULFID 41 52
 FT DISULFID 46 63
 FT DISULFID 65 74
 FT DISULFID 82 163
 FT DISULFID 103 145
 FT DISULFID 134 158
 FT DISULFID 168 299
 FT DISULFID 211 227
 FT DISULFID 219 288
 FT DISULFID 313 388
 FT DISULFID 345 361
 FT DISULFID 378 406
 FT CARBOHYD 139 139
 FT CARBOHYD 352 352
 SQ SEQUENCE 431 AA; 48221 MW; 699B5675B162CBF CRC64;
 Query Match 64.4%; Score 38; DB 1; Length 431;
 Best Local Similarity 66.7%; Pred. No. 9.2;
 Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 2 RLRSGEPOC 10
 DB 280 QLKSGSPQC 288
 RESULT 14
 ID URT2_DESRO STANDARD; PRT; 477 AA.
 AC P15638;

DT 01-APR-1990 (Rel. 14, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Salivary plasminogen activator alpha 2 precursor (EC 3.4.21.68) (DSPA
 alpha-2) (BAT-PA) (T-plasminogen activator).
 OS Desmodus rotundus (Vampire bat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Chiroptera; Microchiroptera; Phyllostomidae;
 OC Desmodontinae; Desmodus.
 OX NCBI_TaxID=9430;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Salivary gland;
 RX MEDLINE=92039036; PubMed=1937019;
 RA Kraetzschmar J., Haendler B., Langer G., Boidol W., Bringmann P.,
 RA Alagon A., Donner P., Schleuning W.D.;
 RT "The plasminogen activator family from the salivary gland of the
 RT vampire bat Desmodus rotundus: cloning and expression.";
 RL Gene 105:229-237(1991).
 RN [2]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC TISSUE=Salivary gland;
 RX MEDLINE=90036867; PubMed=2509450;
 RA Gardell S.J., Duong L.T., Diehl R.E., York J.D., Hare T.R.,
 RA Register R.B., Jacobs J.W., Dixon R.A.F., Friedman P.A.;
 RT "Isolation, characterization, and cDNA cloning of a vampire bat
 RT salivary plasminogen activator.";
 RL J. Biol. Chem. 264:17947-17952(1989).
 RN [3]
 RP CHARACTERIZATION.
 RX MEDLINE=93393059; PubMed=1309059;
 RA Schleuning W.-D., Alagon A., Boidol W., Bringmann P., Petri T.,
 RA Kraetzschmar J., Haendler B., Langer G., Baldus B., Witt W.,
 RA Donner P.;
 RT "Plasminogen activators from the saliva of Desmodus rotundus (common
 RT vampire bat): unique fibrin specificity.";
 RL Ann. N.Y. Acad. Sci. 667:395-403(1992).
 CC -!- FUNCTION: PROBABLY ESSENTIAL TO SUPPORT THE FEEDING HABITS OF THIS
 CC EXCLUSIVELY HAEMATOPHAGOUS ANIMAL. PROBABLE POTENT THROMBOLYTIC
 CC AGENT.
 CC -!- CATALYTIC ACTIVITY: Specific cleavage of Arg-I-Val bond in
 CC plasminogen to form plasmin.
 CC -!- ENZYME REGULATION: ACTIVITY TOWARD PLASMINOGEN IS STIMULATED IN
 CC THE PRESENCE OF FIBRIN I.
 CC -!- SUBUNIT: MONOMER.
 CC -!- DOMAIN: THE FIBRONECTIN TYPE-I DOMAIN MEDIATES BINDING TO FIBRIN,
 CC AND THE KRINGLE DOMAIN APPARENTLY MEDIATES FIBRIN-INDUCED
 CC STIMULATION OF ACTIVITY.
 CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -!- SIMILARITY: CONTAINS 1 EGF-LIKE DOMAIN.
 CC -!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE I DOMAIN.
 CC -!- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
 CC -----
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 CC -----
 DR EMBL; MG3988; AAA31593.1; -;
 DR EMBL; J05082; AAA31596.1; -;
 DR PIR; A34369; A34369.
 DR HSP; P98119; 1A51.
 DR MEROPS; S01.232; -;
 DR InterPro; IPR001314; Chymotrypsin.
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR000083; Fibrinctn1.
 DR InterPro; IPR000001; Kringle.
 DR InterPro; IPR001254; Ser_protease_Try.
 DR Pfam; PF00008; EGF; 1.
 DR Pfam; PF00039; fn1; 1.

DR Pfam; PF00051; kringle; 1.
 DR Pfam; PF00089; trypsin; 1.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00018; KRINGLE.
 DR PRODOM; PD000395; Kringle; 1.
 DR SMART; SM00181; EGF; 1.
 DR SMART; SM00058; FN1; 1.
 DR SMART; SM00130; KR; 1.
 DR SMART; SM00020; Tryp_SPC; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; 1.
 DR PROSITE; PS01253; FIBRONECTIN_1; 1.
 DR PROSITE; PS00021; KRINGLE_1; 1.
 DR PROSITE; PS50070; KRINGLE_2; 1.
 DR PROSITE; PS50240; TRYPSIN_DOM; 1.
 DR PROSITE; PS00134; TRYPSIN_HIS; 1.
 DR PROSITE; PS00135; TRYPSIN_SER; 1.
 KW Plasminogen activation; Hydrolase; Serine protease; Glycoprotein;
 KW Kringle; EGF-like domain; Signal; Multigene family.
 FT SIGNAL 1 36
 FT CHAIN 37 477
 FT DOMAIN 40 82
 FT DOMAIN 83 121
 FT DOMAIN 128 209
 FT DOMAIN 225 477
 FT ACT_SITE 272 272
 FT ACT_SITE 321 321
 FT ACT_SITE 428 428
 FT DISULFID 42 72
 FT DISULFID 70 79
 FT DISULFID 87 98
 FT DISULFID 92 109
 FT DISULFID 111 120
 FT DISULFID 128 209
 FT DISULFID 149 191
 FT DISULFID 180 204
 FT DISULFID 214 345
 FT DISULFID 257 273
 FT DISULFID 334 344
 FT DISULFID 359 434
 FT DISULFID 391 407
 FT DISULFID 424 452
 FT CARBOHYD 185 185
 FT CARBOHYD 398 398
 FT CONFLICT 403 403
 FT CONFLICT 417 417
 FT CONFLICT 435 435
 SQ SEQUENCE 477 AA; 53719 MW; 17486555C0E5077C CRC64;

Query Match 64.4%; Score 38; DB 1; Length 477;
 Best Local Similarity 66.7%; Pred No. 10;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 RLRSGEPC 10

Db 326 QLKSGSPQC 334

RESULT 15

YOAA_ECOLI

ID YOAA_ECOLI STANDARD; PRT; 636 AA.

AC P76257; O07973;

DT 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Probable ATP-dependent helicase yoaa.

GN YOAA OR B1808.

OS Escherichia coli.

OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;

OC Escherichia.

OX NCBI_TaxID=562;

RN [1]

RP SEQUENCE FROM N.A.

```

RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97251358; PubMed=9097040;
RA Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,
RA Kasai H., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T.,
RA Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y.,
RA Nashimoto H., Nishio Y., Oshima T., Saito N., Sempel G., Seki Y.,
RA Sivasubramanian S., Tagami H., Takeda J., Takemoto K., Wada C.,
RA Yamamoto Y., Horiuchi T.;
RT "A 460-kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 40.1-50.0 min region on the linkage map.";
RL DNA Res. 3:379-392(1996).
CC -!- SIMILARITY: BELONGS TO THE HELICASE FAMILY. DING SUBFAMILY.
CC STRONG, TO H.INFLUENZAE HI0387.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC -----
DR EMBL; AE000275; AAC74878.1;
DR EMBL; D90824; BAAL5612.1;
DR EMBL; D90825; BAAL5617.1;
DR EcoGene; EGI3513; yoaA.
KW Hypothetical protein; Hydrolase; Helicase; ATP-binding;
KW DNA-binding; Complete proteome.
FT NP_BIND 45 52 ATP (POTENTIAL).
FT SITE 225 228 DEAH BOX.
FT DOMAIN 193 196 POLY-VAL.
SQ SEQUENCE 636 AA; 70377 MW; 14CEBD04CCBE701F CRC64;

Query Match 64.4%; Score 38; DB 1; Length 636;
Best Local Similarity 75.0%; Pred. No. 14;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRLRSGEP 8
DB 557 CRLRGDP 564

```

Search completed: January 30, 2003, 13:32:17
Job time : 13 secs

GenCore version 5.1.1.3
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OM protein - protein search, using sw model

Run on: January 30, 2003, 13:32:01 ; Search time 29 seconds
(without alignments)
71.051 Million cell updates/sec

Title: US-09-615-624A-1
Perfect score: 59
Sequence: 1 CRLRGEPQC 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 571580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- SPTREMBL_21.*
- 1: sp_archaea.*
 - 2: sp_bacteria.*
 - 3: sp_fungi.*
 - 4: sp_human.*
 - 5: sp_invertebrate.*
 - 6: sp_mammal.*
 - 7: sp_mhc.*
 - 8: sp_organelle.*
 - 9: sp_phase.*
 - 10: sp_plant.*
 - 11: sp_rodent.*
 - 12: sp_virus.*
 - 13: sp_vertebrate.*
 - 14: sp_unclassified.*
 - 15: sp_virus.*
 - 16: sp_bacteriophage.*
 - 17: sp_archaea.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-----------|--------------------|
| 1 | 45 | 76.3 | 3767 | 5 Q9UAI3 | Q9UAI3 caenorhabdi |
| 2 | 42 | 71.2 | 86 | 16 Q9XOE9 | Q9XOE9 neisseria m |
| 3 | 42 | 71.2 | 2091 | 5 Q9VJ69 | Q9VJ69 drosophila |
| 4 | 41 | 69.5 | 798 | 4 Q8WUM6 | Q8WUM6 homo sapien |
| 5 | 40 | 67.8 | 892 | 5 P91085 | P91085 caenorhabdi |
| 6 | 39 | 66.1 | 55 | 16 Q9RKI7 | Q9RKI7 streptomyce |
| 7 | 39 | 66.1 | 66 | 5 Q9NL69 | Q9NL69 caenorhabdi |
| 8 | 39 | 66.1 | 85 | 5 Q9NL71 | Q9NL71 caenorhabdi |
| 9 | 39 | 66.1 | 205 | 4 Q9V4U5 | Q9V4U5 homo sapien |
| 10 | 39 | 66.1 | 127 | 13 Q8QFQ2 | Q8QFQ2 xenopus lae |
| 11 | 38.5 | 65.3 | 127 | 6 Q9TV27 | Q9TV27 nysticebus |
| 12 | 38 | 64.4 | 114 | 4 Q05835 | Q05835 homo sapien |
| 13 | 38 | 64.4 | 157 | 5 Q9V9A1 | Q9V9A1 drosophila |
| 14 | 38 | 64.4 | 368 | 10 Q9XFB9 | Q9XFB9 arabidopsis |
| 15 | 38 | 64.4 | 423 | 4 Q9BPW2 | Q9BPW2 homo sapien |
| 16 | 38 | 64.4 | 435 | 4 Q9BZX8 | Q9BZX8 homo sapien |

| | | | | | |
|----|------|------|------|-----------|---------------------|
| 17 | 38 | 64.4 | 560 | 4 Q9BZY0 | Q9BZY0 homo sapien |
| 18 | 38 | 64.4 | 585 | 4 Q9BZX6 | Q9BZX6 homo sapien |
| 19 | 38 | 64.4 | 611 | 4 Q9BZY3 | Q9BZY3 homo sapien |
| 20 | 38 | 64.4 | 633 | 4 Q9BZX9 | Q9BZX9 homo sapien |
| 21 | 38 | 64.4 | 634 | 16 Q8ZET2 | Q8ZET2 versinlia pe |
| 22 | 38 | 64.4 | 636 | 16 Q8XF32 | Q8XF32 salmonella |
| 23 | 38 | 64.4 | 636 | 16 Q8XDR3 | Q8XDR3 escherichia |
| 24 | 38 | 64.4 | 641 | 4 Q15959 | Q15959 homo sapien |
| 25 | 38 | 64.4 | 646 | 16 Q9KQR8 | Q9KQR8 vibrio chol |
| 26 | 38 | 64.4 | 706 | 13 Q42593 | Q42593 xenopus lae |
| 27 | 38 | 64.4 | 759 | 4 Q9BWP7 | Q9BWP7 homo sapien |
| 28 | 38 | 64.4 | 781 | 4 Q8WUA0 | Q8WUA0 homo sapien |
| 29 | 38 | 64.4 | 797 | 4 Q15156 | Q15156 homo sapien |
| 30 | 38 | 64.4 | 824 | 4 Q9BZY2 | Q9BZY2 homo sapien |
| 31 | 38 | 64.4 | 829 | 4 Q9BZX7 | Q9BZX7 homo sapien |
| 32 | 38 | 64.4 | 854 | 4 Q9BZY1 | Q9BZY1 homo sapien |
| 33 | 37.5 | 63.6 | 127 | 6 Q9TV26 | Q9TV26 eulemur ful |
| 34 | 37.5 | 63.6 | 1515 | 13 Q9DE37 | Q9DE37 brachydanio |
| 35 | 37 | 62.7 | 161 | 17 Q58640 | Q58640 pyrococcus |
| 36 | 37 | 62.7 | 182 | 2 Q46616 | Q46616 erwinia amy |
| 37 | 37 | 62.7 | 234 | 4 Q96IU2 | Q96IU2 homo sapien |
| 38 | 37 | 62.7 | 263 | 4 Q95633 | Q95633 homo sapien |
| 39 | 37 | 62.7 | 337 | 5 Q9VL33 | Q9VL33 drosophila |
| 40 | 37 | 62.7 | 484 | 5 Q22967 | Q22967 caenorhabdi |
| 41 | 37 | 62.7 | 537 | 10 Q9AY52 | Q9AY52 oryza sativ |
| 42 | 37 | 62.7 | 553 | 11 P97543 | P97543 rattus norv |
| 43 | 37 | 62.7 | 793 | 4 Q9H522 | Q9H522 homo sapien |
| 44 | 37 | 62.7 | 798 | 6 Q9GLP0 | Q9GLP0 sus scrofa |
| 45 | 37 | 62.7 | 798 | 6 Q8SQC0 | Q8SQC0 bos taurus |

ALIGNMENTS

RESULT 1

| | | | |
|--------|--|---|----------|
| Q9UAI3 | PRELIMINARY; | PRT; | 3767 AA. |
| ID | Q9UAI3 | Q21340; | |
| AC | Q9UAI3 | Q21340; | |
| DT | 01-MAY-2000 | (TREMBLrel. 13, Created) | |
| DT | 01-MAY-2000 | (TREMBLrel. 13, Last sequence update) | |
| DT | 01-JUN-2002 | (TREMBLrel. 21, Last annotation update) | |
| DE | Transmembrane cell adhesion receptor MUA-3 precursor (K08E5.3 protein) | | |
| DE | (Fragment) | | |
| GN | MUA-3 OR K08E5.3. | | |
| OS | Caenorhabditis elegans. | | |
| OC | Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; | | |
| OC | Rhabditidae; Peloderinae; Caenorhabditis. | | |
| OX | NCBI_TaxID=6239; | | |
| RN | [1] | | |
| RP | SEQUENCE FROM N.A. | | |
| RC | STRAIN=N2; | | |
| RA | Lu Z., Vogel B., Hedgecock E.; | | |
| RT | "mua-3 mRNA Splicing Pattern Revealed." | | |
| RL | Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases. | | |
| RN | [2] | | |
| RP | SEQUENCE FROM N.A. | | |
| RA | Kershaw J.K.; | | |
| RN | Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases. | | |
| RP | [3] | | |
| RN | SEQUENCE FROM N.A. | | |
| RP | MEDLINE-99069613; PubMed-9851916; | | |
| RA | none; | | |
| RT | "Genome sequence of the nematode C.elegans: A platform for | | |
| RT | investigating biology." | | |
| RN | [4] | | |
| RP | SEQUENCE FROM N.A. | | |
| RA | Berks M., Smith A., Lloyd C.R.; | | |
| RN | Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases. | | |
| DR | EMBL; AF139060; AAD29428.1; | | |
| DR | EMBL; Z30974; CAA83226.2; | | |
| DR | EMBL; Z30423; CAA83226.2; JOINED. | | |
| DR | EMBL; Z30423; CAC42345.1; | | |

DR EMBL; 230974; CAC42345.1; JOINED.
 DR HSP; P01130; ILDL.
 DR InterPro; IPR000152; Asx_hydroxyl.
 DR InterPro; IPR001762; Disintegrin.
 DR InterPro; IPR000561; EGF-like.
 DR InterPro; IPR001881; EGF_Ca.
 DR InterPro; IPR002172; LDL_recept_A.
 DR InterPro; IPR000082; SEA_domain.
 DR InterPro; IPR002035; VWF_A.
 DR Pfam; PF00008; EGF; 33.
 DR Pfam; PF00057; ldl_recept_a; 3.
 DR Pfam; PF01390; SEA; 2.
 DR Pfam; PF00092; vwa; 1.
 DR PRINTS; PR00289; DISINTEGRIN.
 DR PRINTS; PR00261; LDLRECEPTOR.
 DR PRINTS; PR00453; VWFADOMAIN.
 DR SMART; SM00179; EGF_CA; 1.
 DR SMART; SM00001; EGF_like; 45.
 DR SMART; SM00192; LDLA; 4.
 DR SMART; SM00200; SEA; 2.
 DR SMART; SM00327; VWA; 1.
 DR PROSITE; PS00010; ASX-HYDROXYL; UNKNOWN_32.
 DR PROSITE; PS00022; EGF_1; UNKNOWN_1.
 DR PROSITE; PS01186; EGF_2; 6.
 DR PROSITE; PS01187; EGF_CA; 1.
 DR PROSITE; PS00068; LDLRA_2; 2.
 DR PROSITE; PS50024; SEA; 4.
 DR PROSITE; PS50234; VWEA; 2.
 KW Calcium-binding; EGF-like domain; Glycoprotein; Receptor; Repeat;
 KW Signal.
 FT SIGNAL.
 FT CHAIN 1 24 POTENTIAL.
 FT FT CHAIN 25 >3767 3.
 FT NON_TER 3767 3767
 FT SEQUENCE 3767 AA; 417284 MW; 8D3A5E5EA50ABE8E CRC64;
 Query Match 76.38; Score 45; DB 5; Length 3767;
 Best Local Similarity 70.08; Pred. No. 9;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 CRLRSGEPQC 10
 DB 2088 CRLMGGEPC 2097
 ID Q9K0E9 PRELIMINARY; PRT; 86 AA.
 AC Q9K0E9;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DE Hypothetical protein NMB0658.
 GN NMB0658.
 OS Neisseria meningitidis (serogroup B).
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
 OX NCBI_TaxID=491;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MC58 / SEROGROUP B;
 RX MEDLINE=20175755; PubMed=10710307;
 RA Tetelin H., Saunders N.J., Heideberg J., Jeffries A.C., Nelson K.E.,
 RA Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,
 RA Nelson W.C., Gwynn M.L., DeBoy R., Peterson J.D., Hickey E.K.,
 RA Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,
 RA Mason T., Clecko A., Parksey D.S., Blair E., Cifton H., Clark E.B.,
 RA Cotton M.D., Utterback T.R., Khouri H., Qin H., Vamathevan J.,
 RA Gill J., Scarlato V., Maignani V., Pizzo M., Grandi G., Sun L.,
 RA Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.,
 RT "Complete genome sequence of Neisseria meningitidis serogroup B strain
 RT MC58.";
 RL Science 287:1809-1815(2000).
 DR EMBL; AE002420; AAF62315.1; -.
 DR

DR TIGR; NMB0658; -.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 86 AA; 9933 MW; 5CEB3DF0A5F8D0E5 CRC64;
 Query Match 71.2%; Score 42; DB 16; Length 86;
 Best Local Similarity 66.7%; Pred. No. 0.83;
 Matches 8; Conservative 2; Mismatches 0; Indels 2; Gaps 1;
 QY 1 CRLR--SGEPQC 10
 DB 24 CRLRMSTGGPQC 35
 ID Q9VJ69 PRELIMINARY; PRT; 2091 AA.
 AC Q9VJ69;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DE CG15165 protein.
 DE CG15165 protein.
 GN CG15165
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Cocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brannon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Aghayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Fostler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalaai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Smith H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Slen T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RT "The genome sequence of Drosophila melanogaster.";
 RL Science 287:2185-2195(2000).
 DR EMBL; AF003659; AAF53685.1; -.
 DR FlyBase; FBgn0032695; CG15165.
 SQ SEQUENCE 2091 AA; 241956 MW; 63AA3D744205AE14 CRC64;
 DR

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Query Match          71.2%; Score 42; DB 5; Length 2091;
Best Local Similarity 88.9%; Pred. No. 20;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRLRSGEPQ 9
DB 1632 CRLRSGEAQ 1640
      |||||
      |||||

RESULT 4
Q8WUM6 PRELIMINARY; PRT; 798 AA.
AC Q8WUM6;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypochemical 88.4 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SKIN;
RA Strausberg R.;
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC020057; AAH20057.1; -.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR002369; Integrin_B.
DR InterPro; IPR001169; Integrin_beta_C.
DR InterPro; IPR003659; Plexin-like.
DR Pfam; PF00362; Integrin_B.1.
DR PRINTS; PR01186; INTEGRINB.
DR ProDom; PD001811; Integrin_B.1.
DR SMART; SM00187; INB; 1.
DR SMART; SM00423; PSI; 1.
DR PROSITE; PS00022; EGF_1; UNKNOWN_2.
DR PROSITE; PS00243; INTEGRIN_BETA; UNKNOWN_3.
KW Hypochemical protein.
SQ SEQUENCE 798 AA; 88415 MW; DE35979C1625578C CRC64;

Query Match          69.5%; Score 41; DB 4; Length 798;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RLRSGEPO 9
DB 122 RLRSGEPO 129
      |||||
      |||||

RESULT 5
P91085 PRELIMINARY; PRT; 892 AA.
AC P91085;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypochemical 99.7 kDa protein.
GN F5A12.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX MEDLINE=99069613; PubMed=9851916;
RA None.
RT "Genome sequence of the nematode C. elegans: a platform for
investigating biology. The C. elegans Sequencing Consortium.";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.

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```

RC STRAIN=BRISTOL N2;
RA Pauley A., Gattung S.;
RT "The sequence of C. elegans cosmid F5A12.";
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RA Waterston R.;
RT "Direct Submission.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF003130; AAB94129.1; -.
DR InterPro; IPR003100; PAZ.
DR InterPro; IPR003165; Plwi.
DR Pfam; PF02170; PAZ; 1.
DR Pfam; PF02171; Plwi; 1.
KW Hypochemical protein.
SQ SEQUENCE 892 AA; 99749 MW; 44FE58335244DE3E CRC64;

Query Match          67.8%; Score 40; DB 5; Length 892;
Best Local Similarity 60.0%; Pred. No. 21;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRLRSGEPQ 10
DB 511 CRFSSGDPQC 520
      |||||
      |||||

RESULT 6
Q9RK17 PRELIMINARY; PRT; 55 AA.
AC Q9RK17;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypochemical protein SC03445.
GN SC03445 OR SCE46.02C.
OS Streptomyces coelicolor.
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neil S.,
RA Rabinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
coelicolor A3(2)";
RL Nature 417:141-147(2002).
DR EMBL; AL133252; CAB61853.1; -.
KW Hypochemical protein.
SQ SEQUENCE 55 AA; 5927 MW; BF89F887A528D263 CRC64;

Query Match          66.1%; Score 39; DB 16; Length 55;
Best Local Similarity 70.0%; Pred. No. 2.1;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRLRSGEPQ 10
DB 4 CLARSGFPQC 13
      .|||
      .|||

RESULT 7
Q9NL69 PRELIMINARY; PRT; 66 AA.
AC Q9NL69;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)

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DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE ABF-2 (Fragment).
 GN ABF-2.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kato Y.;
 RT "a polycistronic precursor RNA for abf operon in Caenorhabditis
 RT elegans.";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB029811; BAA89492.1; -
 FT NON_TER 66 66
 SQ SEQUENCE 66 AA; 7017 MW; E845F57F53FAA689 CRC64;
 Query Match 66.1%; Score 39; DB 5; Length 66;
 Best Local Similarity 60.0%; Pred. No. 2.5;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 1 CRLRSRGPQC 10
 Db 55 CKKRSRGPQC 64
 RESULT 8
 Q9NL71
 ID Q9NL71 PRELIMINARY; PRT; 85 AA.
 AC Q9NL71;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE ABF-2 precursor (Hypothetical 8.9 kDa protein).
 GN ABF-2 OR C50F2.10.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Kato Y.;
 RT "ABF-2, an ASABF-type antimicrobial peptide in Caenorhabditis
 RT elegans.";
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB029811; BAA89492.1; -
 FT NON_TER 66 66
 SQ SEQUENCE 66 AA; 7017 MW; E845F57F53FAA689 CRC64;
 Query Match 66.1%; Score 39; DB 5; Length 66;
 Best Local Similarity 60.0%; Pred. No. 2.5;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 1 CRLRSRGPQC 10
 Db 55 CKKRSRGPQC 64
 RESULT 9
 Q9Y4U5
 ID Q9Y4U5 PRELIMINARY; PRT; 205 AA.
 AC Q9Y4U5;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Hypothetical 21.5 kDa protein (Fragment).
 GN DKFZP586I11.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ottensvaelder B., Obermaier B., Mewes H.W., Gassenhuber J., Wiemann S.;
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL050131; CAB43283.2; -
 FT NON_TER 1 1
 SQ SEQUENCE 205 AA; 21548 MW; D88EB7A823C618E4 CRC64;
 Query Match 66.1%; Score 39; DB 4; Length 205;
 Best Local Similarity 75.0%; Pred. No. 7.7;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 3 LRSRGPQC 10
 Db 170 LRAGDPQC 177
 RESULT 10
 Q8QFQ2
 ID Q8QFQ2 PRELIMINARY; PRT; 285 AA.
 AC Q8QFQ2;
 DT 01-JUN-2002 (TREMBLrel. 21, Created)
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Mig30.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Piploidea; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=ANTERIOR ENDOMESODERM OF THE SPEMANN ORGANIZER, AND ENDODERM;
 RX MEDLINE=21839545; PubMed=11850177;
 RA Hayata T., Tanegashima K., Takahashi S., Sogame A., Asashima M.;
 RT "Overexpression of the secreted factor Mig30 expressed in the Spemann
 RT organizer impairs morphogenetic movements during Xenopus
 RT gastrulation.";
 RL Mech. Dev. 112:37-51(2002).
 DR EMBL; AB035379; BAB84702.1; -
 SQ SEQUENCE 285 AA; 31431 MW; 346295C6C77B6BE0 CRC64;
 Query Match 66.1%; Score 39; DB 13; Length 285;
 Best Local Similarity 57.1%; Pred. No. 11;
 Matches 8; Conservative 1; Mismatches 1; Indels 4; Gaps 1;
 QY 1 CRLRSQ----EPOC 10
 Db 92 CQLRGHVNPEQC 105

Query Match 66.1%; Score 39; DB 5; Length 85;
 Best Local Similarity 60.0%; Pred. No. 3.2;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 1 CRLRSRGPQC 10
 Db 55 CKKRSRGPQC 64
 RESULT 9
 Q9Y4U5
 ID Q9Y4U5 PRELIMINARY; PRT; 205 AA.
 AC Q9Y4U5;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Hypothetical 21.5 kDa protein (Fragment).
 GN DKFZP586I11.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ottensvaelder B., Obermaier B., Mewes H.W., Gassenhuber J., Wiemann S.;
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL050131; CAB43283.2; -
 FT NON_TER 1 1
 SQ SEQUENCE 205 AA; 21548 MW; D88EB7A823C618E4 CRC64;
 Query Match 66.1%; Score 39; DB 4; Length 205;
 Best Local Similarity 75.0%; Pred. No. 7.7;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 3 LRSRGPQC 10
 Db 170 LRAGDPQC 177
 RESULT 10
 Q8QFQ2
 ID Q8QFQ2 PRELIMINARY; PRT; 285 AA.
 AC Q8QFQ2;
 DT 01-JUN-2002 (TREMBLrel. 21, Created)
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Mig30.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Piploidea; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=ANTERIOR ENDOMESODERM OF THE SPEMANN ORGANIZER, AND ENDODERM;
 RX MEDLINE=21839545; PubMed=11850177;
 RA Hayata T., Tanegashima K., Takahashi S., Sogame A., Asashima M.;
 RT "Overexpression of the secreted factor Mig30 expressed in the Spemann
 RT organizer impairs morphogenetic movements during Xenopus
 RT gastrulation.";
 RL Mech. Dev. 112:37-51(2002).
 DR EMBL; AB035379; BAB84702.1; -
 SQ SEQUENCE 285 AA; 31431 MW; 346295C6C77B6BE0 CRC64;
 Query Match 66.1%; Score 39; DB 13; Length 285;
 Best Local Similarity 57.1%; Pred. No. 11;
 Matches 8; Conservative 1; Mismatches 1; Indels 4; Gaps 1;
 QY 1 CRLRSQ----EPOC 10
 Db 92 CQLRGHVNPEQC 105

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RESULT 11
Q9TV27 ID Q9TV27 PRELIMINARY; PRT; 127 AA.
AC Q9TV27;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Ribonuclease k6 (Fragment).
OS Nycticebus coucang (slow loris).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Strepsirrhini; Loridae; Nycticebus.
OX NCBI_TaxID=9470;
RN [1]
RP SEQUENCE FROM N.A.
RA Deming M.S., Dyer K.D., Seekamp R.L., Rosenberg H.F.;
RT "Evolution of three primate ribonuclease genes: comparative analysis
RT of RNase 4, RNase k6, and RNase 2 (eosinophil-derived neurotoxin).";
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF078123; RAD48537.1; -
DR HSP; P00656; 2RNS.
DR InterPro; IPR001427; RNaseA.
DR Pfam; PF00074; RNaseA; 1.
DR PRINTS; PR00794; RIBONUCLEASE.
DR ProDom; PD000535; RNaseA; 1.
DR SMART; SM00092; RNase_PC; 1.
DR PROSITE; PS00127; RNASE_PANCREATIC; UNKNOWN_1.
FT NON_TER 127
FT SEQUENCE 127 AA; 14611 MW; 76F16ED9107DD66F CRC64;

Query Match 65.3%; Score 38.5; DB 6; Length 127;
Best Local Similarity 72.7%; Pred. No. 6;
Matches 8; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 1 CRLRSGE-PQC 10
DB 81 CRLTSKYPQC 91

RESULT 12
Q05835 ID Q05835 PRELIMINARY; PRT; 114 AA.
AC Q05835;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Promyelocytic leukemia protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=93116464; PubMed=8380300;
RA Geng J.P., Tong J.H., Dong S., Wang Z.Y., Chen S.J., Chen Z.,
RA Zelen A., Berger R., Larsen C.J.;
RT "Localization of the chromosome 15 breakpoints and expression of
RT multiple PML-RAR alpha transcripts in acute promyelocytic leukemia: a
RT study of 28 Chinese patients.";
RL Leukemia 7:20-26(1993).
DR EMBL; S51489; AAD13865.1; -
DR NON_TER 1
DR SEQUENCE 114 AA; 12861 MW; 11E9933161535F8D CRC64;

Query Match 64.4%; Score 38; DB 4; Length 114;
Best Local Similarity 77.8%; Pred. No. 6.8;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CRLRSGE-PQC 9
DB 53 CRLRQEPQ 61

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RESULT 13
Q9V9A1 ID Q9V9A1 PRELIMINARY; PRT; 157 AA.
AC Q9V9A1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE CG15235 protein.
GN CG15235.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=BERKELEY;
RX MEDLINE=20195006; PubMed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkuch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzby D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT "The genome sequence of Drosophila melanogaster.";
RL Science 287:2185-2195(2000).
DR EMBL; AE003790; AAF57395.1; -
DR FlyBase; FBgn003103; CG15235.
DR InterPro; IPR000595; cNMP_binding.
DR Pfam; PF00027; cNMP_binding; 1.
DR PROSITE; PS50042; cNMP_BINDING_3; 1.
DR SEQUENCE 157 AA; 17664 MW; 46EBCB9F416D032B CRC64;

Query Match 64.4%; Score 38; DB 5; Length 157;
Best Local Similarity 70.0%; Pred. No. 9.3;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRLRSGE-PQC 10
DB 27 CRLRRVEPLC 36

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RESULT 14
Q9XFB9
ID Q9XFB9 PRELIMINARY; PRT; 368 AA.
AC Q9XFB9;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Zinc finger protein 3.
GN ZFN3
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLOMBIA;
RA Choi S., Lee J., Yi H., Shin B., Choi G.;
RT "Characterization of zinc finger protein 3 (ZFN-3) in Arabidopsis
thaliana.";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RX MEDLINE=97471969; PubMed=9330910;
RA Sato S., Kotani H., Nakamura Y., Kaneko T., Asamizu E., Fukami M.,
RA Miyajima N., Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. I. Sequence
features of the 1.6 Mb regions covered by twenty physically assigned
Pl clones.";
RL DNA Res. 4:215-230(1997).
DR EMBL; AF138872; AAD27875.1; -.
DR EMBL; AB005242; BAB09623.1; -.
DR InterPro; IPR000571; Znf_CCCH.
DR Pfam; PF00642; zf-CCCH; 5.
DR SMART; SM00356; Znf_C3H1; 5.
SQ SEQUENCE 368 AA; 40792 MW; 84EFCAAADB18A15C CRC64;

Query Match 64.4%; Score 38; DB 10; Length 368;
Best Local Similarity 70.0%; Pred. No. 22;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRLRSGEPQC 10
Db 279 CVLSGEPQC 288
I I I I I I I I

RESULT 15
Q9BPW2
ID Q9BPW2 PRELIMINARY; PRT; 423 AA.
AC Q9BPW2;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Tripartite motif protein TRIM19 Iota (Tripartite motif protein TRIM19
eta).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92278759; PubMed=1594241;
RA Fagioli M., Alcalay M., Pandolfi P.P., Venturini L., Mencarelli A.,
RA Simeone A., Acampora D., Grignani F., Pellicci P.G.;
RT "Alternative splicing of PML transcripts predicts coexpression of
several carboxy-terminally different protein isoforms.";
RL Oncogene 7:1083-1091(1992).
[2]
RP SEQUENCE FROM N.A.
RA Reymond A., Meroni G.;
RT "Deciphering the function of the Tripartite Motif containing

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proteins.";
RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Fagioli M., Reymond A., Meroni G.;
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA Reymond A., Meroni G.;
RT "Deciphering the function of the Tripartite Motif containing
proteins.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.
DR EMBL; AF230409; AAG50188.1; -.
DR EMBL; AF230407; AAG50186.1; -.
DR HSP; P29590; IBOR.
DR InterPro; IPR000315; Znf_Bbox.
DR InterPro; IPR001841; Znf_ring.
DR Pfam; PF00643; zf-B_box; 2.
DR Pfam; PF00097; zf-C3HC4; 1.
DR SMART; SM00336; BBOX; 1.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS00518; ZF_RING_1; 1.
KW Zinc-finger.
SQ SEQUENCE 423 AA; 47574 MW; EE5031BE9C3B33C8 CRC64;

Query Match 64.4%; Score 38; DB 4; Length 423;
Best Local Similarity 77.8%; Pred. No. 25;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CRLRSGEPQ 9
Db 357 CRLRQEPQ 365
I I I I I I I I

Search completed: January 30, 2003, 13:34:19
Job time : 31 secs

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